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February 14, 2004, 14:10:20; Search time 2707 Seconds (without alignments) 7994.530 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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Shirton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, L., Bastien, V., Beda, F., Boqusiavkiy, L., Anderson, S., Barna, M., Bastien, V., Beda, F., Boqusiavkiy, L., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Daz, J.S., Dodge, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grand-Pierre, N., Hagos, B., Haeford, A., Horton, L., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonad, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., Marduis, N., McCarthy, M., McEwan, P., McKernan, K., Morlow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Tesfaye, S., Theodore, J., AC079200 117978 bp DNA linear PRI 01-MAY-2002 Momo sapiens chromosome 8, clone RP11-1058B24, complete sequence. Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 117978)
Birren, B., Linton, L., Nusbaum, C. and Lander, B.
Homo sapiens chromosome 8, clone RP11-1058B24 AC079200.6 GI:20377011 (bases 1 to 117978) Homo sapiens (human) Homo sapiens Unpublished AC079200 DEFINITION ACCESSION ORGANISM AUTHORS TITLE JOURNAL RESULT 1 AC079200 KEYWORDS SOURCE REFERENCE REFERENCE AUTHORS VERSION

Location/Qualifiers 1. .117978

FEATURES

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Shirren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L., Chanderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Chopel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Garcis, S., Gorder, P., Petzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gordere, R., Graham, L., Grand, Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliav, I., Johnson, R., Jones, C., Landera, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landeran, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Marquis, N., Matthews, C., Nicol, K., Milov, J., Marquis, N., Matthews, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Norbu, C., Peterson, K., Phurphy, T., O'Connell, P., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santes, R., Schauer, S., Schuback, R., Senace, S., Schuback, R., Senace, S., Theodore, J., Tophan, K., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Wol, A., Wilson, B., Wand, D., Ye, W. J., Young, G., Shihmitted, O'Llaba, Annatien, A., and Zody, M. Torrish, P., Willer, R., Shihmitted, J., Shihmitte Higher of the control Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (23.3-WG-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 117978) Submitted (21-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 117978) Submitted (01-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On MAY 1, 2002 this sequence version replaced gi:20128014.
All repeats were identified using RepeatMasker: ------ Genome Center Center: Whitehead Institute/ MIT Center for Genome Research Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Center code: WIBK
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu Center project name: L10839 Center clone name: 1058_B_24 TITLE JOURNAL TITLE JOURNAL REFERENCE TITLE JOURNAL REFERENCE AUTHORS COMMENT

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Submitted (14-FBB-2000) Whitehead Institute/MIT Center for Genome Submitted (14-FBB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 3.20 Charles Street, Cambridge, MA 02141, USA

Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazo, D., Chard, T., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gard, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, J., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., McZatthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schubback, R., Seaman, S., Sewery, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Zembek, L., Zimmer, A. and Zody, M., Vandy, M., Vola, Wulsh, M., Wilson, B., Wulx, M., Waman, D., Young, G., Zainoun, J., Direct Submission
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Direct Summission

Exesarch, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

E (Dasses 1 to 167118)

Birren, B., Nusbaun, C., Lander, E., Ali, A., Allen, N., Anderson, S.,

Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B.,

Camarata, J., Chang, J., Chazaro, B., Chopebl, Y., Collymore, A.,

Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S.,

Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,

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Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C.,

McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V.,

Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H.,

O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K.,

Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,

Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,

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Zembek, L., Zimmer, A. and Zody, M.
                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. (basea 1 to 167118)
Birren, B., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone RP11-675P19
                                                                                                                                                                                                           Unpublished
2 (bases 1 to 167118)
   ORGANISM
                                                                                                                                  AUTHORS
TITLE
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Submitted (31-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 31, 2002 this sequence version replaced gi:21699264.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                   Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
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ement(187==
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[ement(1075)
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complement(17909..18160)
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complement (1592. .1655)
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complement (1860, .2187)
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Center clone name: 675_P_19
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baraa, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brana, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Collins, S., Collymore, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferretra, P., Fitzhugh, W. Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Crand. P., Gardyna, S., Ginde, S., Goyette, M., Crand. L., Johnson, R., Hagos, B., Heaford, A., Horton, L., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., Morcarthy, M., McEwan, P., McKernan, K., Morphy, T., Maylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T., Norman, C.H., O'Lover, T., Peterson, K., Fisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Schauers, S., Scherry, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Wilson, B., Wu, X., Whiman, D., Ye, W.J., Young, G., Zainoun, J., Sidnama, J., Markers, A., Talamas, J., Young, G., Zainoun, J., Sidnama, J., Wilson, W., Submission
                                                                                                                                                                                                                                                                             149822 CGGCTGCTTGCCTGCTCCATCACAGGAAGGTGCAGCAGAGCCCTTTTTCTTCCACCAGGCTTG 149763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACU84244 63888 bp DNA linear HTG 18-OCT-2000
Homo sapiens chromosome 8 clone CTD-2240Ll map 8, LOW-PASS SEQUENCE
SAMPLING
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 63888)
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                                                                                                                                                                                                                                             420 AAGCTGTTCGGGGACTTCCAGAATAAACCAAACCAGCTGTATTACTGGTCTTTGACATCC
                                                                                                                                                                                                                                                                                                                                                                  480 TCTCTGGTCAGGCCAAGTCACTGTCCCTGTCTTGGAGAGGCTTCTGAG 529
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence submissions@genome.wi.mit.edu
Contact: Project Information
Center project name: Lil1091
Center clone name: 2240_L_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (Dases 1 to 0,000).
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 8, clone CTD-224011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WIBR
Web site: http://www-seg.wi.mit.edu
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HTG; HTGS PHASE0.
Homo sapiens (human)
Homo sapiens
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / TPL family="CT-rich"

complement (31074. 31316)

/ TPL family="Aluub"

31677. 31770

/ TPL family="MIR"

3166. 32193

/ TPL family="AT rich"

complement (32364. 32699)

/ TPL family="AT rich"

complement (32363. 33657)

/ TPL family="Aluex"

complement (3353. 33757)

/ TPL family="Aluex"

complement (3353. 33744)

/ TPL family="Aluex"

complement (3367)

/ TPL family="Aluex"

33793. 33794.
                                                                                                           / rpt family="1.2785" / rpt family="1.2785" / rpt family="1.1P4" / rpt family="1.1MD1" / rpt family="1.1MD1" / rpt family="1.275" / rpt family="1.275" / rpt family="1.275" / rpt family="1.25190" / rpt famil
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complement (26510. .26818)

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/rpt family="MR"

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/rpt family="LiPAlo"

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/rpt family="LiPAlo"

/rpt family="LiPAlo"
                                                family="LiMC2"
ement(2:21724)
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complement (21284. .21671) / rpt_family="MLT1A1"
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36771. .36797
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/rpt_family="AT_rich"
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contig of 679 bp in length gap of 100 bp in length

53106:

gap of 100 by contig of 692 by in length gap of 100 by contig of 692 by in length gap of 100 by contig of 671 by in length gap of 100 by contig of 671 by in length gap of 100 by contig of 673 by in length gap of 100 by contig of 683 by in length gap of 100 by contig of 683 by in length gap of 100 by contig of 683 by in length gap of 100 by contig of 683 by in length gap of 100 by contig of 683 by in length gap of 100 by contig of 683 by in length gap of 100 by contig of 683 by in length gap of 100 by contig of 684 by in length

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IMDIMHKYTNDNRLALKAGFTMILYSSSIGFLLLFYANFLDLSEKKENDDLIELEEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="asparagine-rich C terminal; Pfam match to PF00083, Sugar (and other) transporter

11 probable transmembrane helices predicted for PF10785c by TMHMM2.0 at as 488-870, 877-896, 901-923, 936-958, 978-1000, 1163-1185, 1200-1222, 1243-1265, 1269-1291, 1304-1326 and 1341-1360"
Submitted (20-SEP-2002) P.falciparum Genome Sequencing Consortium, The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A, UK
For more information about this sequence or the Malaria Project, see http://www.aanger.ac.uk/Projects/P_falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /hote="ProfileScan hit to PS50223, Thioredoxin-domain (does not find all). Similarity to Plasmodium falciparum thoredoxin trx TR:Q9NFK9 [EMBL:AJ277839] (104 as) fasta scores: E(): 9.3e-06, 29.670% id in 91 as. Similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      jdin(9491. .9535,9582. .9722,9830. .9973,10080. .10148)
/gene="PPI0790w"
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969. .1469
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/gene="PFI0785c"
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                                                                                             COMMENT
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Eukaryottam; Apicomplexa; Haemosporida; Plasmodium.

Eukaryottam; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 341050)

1 (bases 1 to 541050)

1 (bases 1 to 5
                                                                                                                                                                                                                                                                                                                                                                                                                                            29687 TCGGGTATATTTTGGAAGTTGTAAAATACTACGTGTTCTCTTCTAAGTCCCACTCCTCTG 29746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29507 CARGGIGAIGCIGIAGICGIGGCIGAITIAIAIGCIGAITIAIGGGIGAITITIGCIICCI 29566
                                                                                                                                                                                                                                                                                                                           29567 TCTTTATACTTTTATTTTTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAAT 29626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFA929357 341050 bp DNA linear INV 29-JAN-2003
Plasmodium falciparum strain 3D7, chromosome 9; segment 3/5.
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Sanders,M., Hauser,H., Baker,S., Unwin,L., Mungall,K., Berriman,M.,
Pain,A., Hall,N., Bowman,S., Churcher,C., Quail,M. and Barrell,B.
Direct Submission
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                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 TCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTCTAAGTCCCACTCCTCTG 239
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                                                                                                                                                      9
                                                                                                                                                                                                                                                                         TCTTTATACTTTTATTTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAAT
                                                                                                                                                                                                                                                                                                                                                                                             aaattatcaaaagaaaaaaactgaaagcaacgcttgaaaaaaaggaaagttag-cccta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 TTTTCTTTGAGCAGGAAAGAGAAAGCAGTCACCCTCTCTTCCATGACAACAACAAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGCACCTTGAACTATCCTGGCTTGCTAGCTAAGAAACTGCCCCAAGTGACGCACACTC
                                                                                                                                                      1 CATGGTGATGCTGTAGTCGTGGCTGATTTATATGCTGATTTATGGTGATTTTGCTTCCT
                                                                                             Gaps
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Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13
Nature 419 (6906), 527-531 (2002)
                                                                                             1,
                                     Length 63888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29927 AAGCTGTTCGGGGACTTCCAGAATAAACCAAACCAGCTGTATTA 29970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      420 AAGCTGTTCGGGGACTTCCAGAATAAACCAAACCAGCTGTATTA 463
                                                                                          Indels
                                  Score 451.6; DB 2;
Pred. No. 1.2e-89;
1; Mismatches 0;
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AL929357.1 GI:23505059
                               tch 85.4%; al Similarity 99.6%; 462; Conservative 1
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                                  Query Match
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PFA929357/c
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EYILTINKALIEKNITITEREFYKYILVALIDDIGFEKNYASQRADYALNYDDKYTKOSILISG
ERINHPHNILHDIDINNERNALIKULDYNYDDYANLAKYDITLEGEDOKYILLHYYL
LIDIFKHMODMKIKIKILYIYVYENIDOYIIRKYRANEKLITHNYKEQNISINDT
DORNIEKLAKOKKFYNDKHHEDETUDSRAGQIDDMHKQRANTKAKKLFLLLGILLEQLR
NILLELYKANYEKNININKKYEETLDEERRESTYNYNKITKAKKEFILLILGILLEQLR
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IKRIFNKLOTLNHNIIIDMNILYNWREKELDISSONNYNDTSHESKNESYDNSHDALSY
IKRIFNKLOTLNHNIIIDNNILYNWREVELDESTYNYTILGSLAKSNNYFNIYYIDE
LSKHFHKYOTLNHNIIIDNNILYNWREVELDESTYNYTNIYYYDNNIYENDYYWYDM
NRENKYISNNIGOYYNDKIKKKNANNYLEDOYNNWREPLDKEIIKKNNNIYENDYYWYDM
NRENKYISNNIGOYYNDKIKKNANNYLEDOYNNWREPLDKEIIKKNNNIYENDYYWYDM
NRENKYISNNIGOYYNDKIKKKNANNYLEDONNNNILLINNNNILYNNNIYTRONNYLYNNNI
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FESHACKNENVALPQINYNASKGKEFTRNWEKQLCHGINFLKNYLLITFIVGIIDLIV
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THYLHAGFYILLADFLTHFIIYIFLKRDKTILKYVCELELIPWDEKKLPVHYAEFUD
TLISPNEITNYLQGLPQQDNINEEQLKNFFGTDNYEQIYYVILNNLKNQKQMMNITPM
Gallus gallus thioredoxin txN SWALL:THIO CHICK (SWALL:P08629) (104 aa) fasta scores: E(): 1.6e-05, 28.57% ain 10.5 aa, and to Ophiophagus hannah thioredoxin txN SWALL:Q98YX1 (SWBL:ARB:AR321769) (105 aa) fasta scores: E(): 1.3e-08, 36.44% id in 107 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Signal anchor predicted for PF10795w by SignalP 2.0 HMM (Signal peptide probabilty 0.152, signal anchor probability 0.803) with cleavage site probability 0.079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEQKANPEKEKSKKUKANNNMKANTFYYSNIYIKCYTHMKSVQKPIYIYTYDKMKH
YFNEYTNYILKKWKKKSFISFYFKQPVILSEIKEQAGNNAIDVENILQNYRLPFVNLE
NFKLYIDDIVSYKQKNVYHIKINTPYKTFMSYQKDHFPYMSHNNVVKYLCIDFSKI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="mgnkmlltkkdknglkkavyiflililipydgwspplvyspcin
krspvlnsigkndngpkyrirdngktilleigwsikegnvskalanldelflaapddkk
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                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MKCYEMINMIHINIYLEQSIYIELKNTGSLNQVFSSTQNSSIVI
KFGAVWCKPCNKIKEYFKNQLNYYYVTLVDIDVDIHPKLNDQHNIKALPTFEFYFNLN
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15947. .16143,16443. .16553,16671. .16777,16874. .16928))
/gene="PFI0800c"
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15947. .16143,16443. .16553,16671. .16777,16874. .16928))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between residues 40 and 41
1 probable transmembrane helix predicted for PFI0795w by TMHMM2.0 at as 21-43"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="No Pfam hit, SMART hit to SM00184, Ring finger"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /hote="4 probable transmembrane helices predicted for PF10800c by TMHMM2.0 at aa 7-29, 88-110, 130-152 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEWVLVHTVEGANQNDIEKAFQKYCLEKAK"
join(10913. .11086,11363. .14623)
/gene="PFI0795w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(10913. .11086,11363. .14623)
/gene="PFI0795w"
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|gene="PFI0805w"
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|gene="PFI0805w"
                                                                                                                                                                                                                                                          product="thioredoxin, putative"
protein id="CAD51844.1"
/db xref="G1:23505062"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="hypothetical protein"
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/db_xref="G1:23505063"
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/db_xref="GI:23505064"
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/protein_id="CAD51847.1"
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Eukaryotta, Alvediata, Apicomplexa, Haemosporida, Plasmodium.

[ bases 1 to 25151]

[ dardnor, M.J. Hang, R. White, O., Berriman, M., Hyman, R.W.,
Gardnor, M., Pain, A., Nelson, K.E., Bowman, S., Paulsen, I.T.,
James, K., Eisen, J.A., Rutherford, K., Salzberg, S.L., Craig, A.,
Kyes, S., Chan, M.S., Nene, V., Shallon, S.J., Suh, B., Peterson, J.,
Angiuoli, S., Petrea, M., Allen, J., Selengut, J., Haft, D.,
Mather, M.W., Vaidya, A.B., Martin, D.M., Faitlamb, A.H.,
Fraunholz, M.J., Roos, D.S., Ralph, S.A., McFadden, G.I.,
Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C.,
Barrell, B.
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                                                                     NHLIKNLCMNCSENMIAFMDNMDSLYFINLANNIINKGLHKNVIFISNDIYEKGYNYN
NIDYNNDREIDRLSVDFTYNKLNKKKKKMYDMNKKDNIINVIISDEIMKYNIKNLTT
FCINPYYNNNNNNNNICVLTNKKTVSLIYIYEYHINSVLLFKDDNILNIYMYESFIF
                                                                                                                                     RPWTIEEIFYEFMLERKNTNIIYKKNIMIKKKKCSTYKKNRLSIILKELRKDKKNRKE
THUUVEKLIYHEKKNKKYYIAAKIFIMWTYLDMKEKNIYIIKMFIITIAEY
YTKLKYALQNKQHGCFKRKKIKKNKHAIYNINRTIFLTTNDLSMKDOKERYYNTIRV
SKKLNIKINFKLKIERNVNKLVYIKHNNIINPQIKYITLIKMKKKNKIKSMLYIFC
                                                                                                                                                                                                                                                                                                                                                                                                       AE014844 251551 bp DNA linear INV 11-FEB-2003
Plasmodium falciparum 3D7 chromosome 12, section 1 of 9 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 419 (6906), 498-511 (2002)
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Hyman, R.W., Fung, E., Conway, A., Kurdi, O., Mao, J., Miranda, M., Makao, B., Rowley, D., Tamaki, T., Wang, F. and Davis, R.W.
Direct Submission
Submitted (13-SEP-2002) Stanford Genome Technology Center, Stifuliversity, 855 Callfornia Avenue, Palo Alto, CA 94304, USA 3 (bases 1 to 251551)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hyman, R.W., Fung, E., Conway, A., Kurdi, O., Mao, J., Miranda, M.,
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Best Local Similarity 57.8%; Pred. No. 0.0098;
Matches 104; Conservative 0; Mismatches 7
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Plasmodium falciparum 3D7
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AE014844 AE014188
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n 1274413048 /rpt_type=tendem n 1282813048 /rpt_type=tendem n 129251310 /rpt_type=tendem n 1304113636 /rpt_type=tendem n 1304913253			n 1362. 14053 /rpt_type=tandem on 13954. 14071			ч /ч.		14590 /rpt 14744	\		л\ _п	-	/rpc cype=tandem <16973>2497 /locus rac=ppp.nnnsw=	join(1697)	join(16973, .22048,23037, .24497) /locus tag="PPL0005w"	/note="HWMPfam hit to PP03011, Plasmodium falciparum erythrocyte mmbrane protein (PPEMP), score 1.4e-64" //odo. graft=1	/product==erythrocyte membrane protein 1 (PfEMP1)" /protein_id="AANA6090.1"	/ VO. XECE="GIT 1249 b 3.2" / LTAIRBLALION="MGPDAVTDYSKATNVKYLPDLIGETVQKKAKEKADVASRKYFE ELHGDLSKATYKKDKNPEGTTPPNPCKLEYQYHTNVTKGEDKEYPCLGRKTVRPSDKE	GABCYKTKI KOSTIDIVGACAPYRRLYMCDRNLEH EPTKI THNLLLDVCLAAQYEG QSI SQMHGKHQLSYPDSPSQLCTELARSFADI GDI VRGRDLYRGNNRENDRKLEKKLKG V PKKT YNNI, VRKKKRERAFTDYKDNA DDPVOI, REDWAJ, NRODYWKA I TCDAAHNSPYRK	MGADGS TESSANROCRUADVPTNEDYPOYLEWFEEWAEPCKKRRHKLKDA IOKCR GODGTGKORYCDIARYDCKRTISAKHELVOGEECKKCSVVCI PFGPWI DNOKOBFEKO	KNKYTNEINKKHDETTKEISGNRRKKRSLTTKNYKGYDEBPYKIPKDBYPDVDKPLDL LSKETAGESOPYDEPRIISINPKNYKNPDIPSHTBYCOACPWCGMTCTPDGKCTKNPE	ELCHHKIVQKEYPDTNTTDIPILTPDTTKSNIVEKYRNPCNSSDDNNSDQINNWQCHY DESKKSGQNDNCVEGTWQNPKKDQKVTSYNAPPWKWVSEMLDDSIKWRABLDKCLKND	KKTCGKKKCNRDCKCFKKKVBQKKEKEWIKAIKKHFKKQKDAIETGMPEMALKTLIND VPLQDMEKAQGDPQHIAKIKELLKKNDEKVNNLSNMETIFDFLLQEEEQDAQKCVSNN
repeat_region repeat_region repeat_region repeat_region	repeat_region	repeat_region repeat_region	repeat_region repeat_region	repeat_region	repeat_region	repeat_region repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region repeat_region	repeat_region	gene	mRNA	cos								
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Nakao, B., Rowley, D., Tamaki, T., Wang, F. and Davis, R.W. Direct Submission Submitted (29-JAN-2003) Stanford Genome Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA Location/Qualifiers 1251551 / organism="Plasmodium falciparum 3D7" // mol type="genomic DNA" // isolate="3D" // db_aref="and" // db_aref	/ cntchosome= 12 ** 4 . 647 / rpt_type=tandem 656 . 797	/Ipt_type=tandem 754933 /rpt_type=tandem 775807	/rpt_type=tandem 20092796 /rpt_type=tandem	/rpt_type=tandem 3622.3748 /rpt type=tandem	9569 - 3734 /rpt_type=tandem 9066 . 9276	<pre>/rpt_type=tandem 90669140 /rpt_type=tandem</pre>	9220. /rpt_type=tandem 93749469	/rpt_type=tandem 9374- 1945. /rpt_type=tandem	9550 .9629 /rpt-type-tandem 9550 .961	/rpt_type=tandem 95509593	/rpc-type=tandem 9670. 110794 /rpt_type=tandem	96949746 from type=tandem from the type=tandem	9/3210260 /rpt_type=tandem 9837. 9899	/rpt_type=tandem 9891	/rpt_type=tandem 1018910254	/rpt_type=tandem 10243. :1081 /rpt_tyme=tandem	10893 . 1094 Xpt type=tandem 1075	11078 . 12485 /rpt type-tandem 11078 . 12488	/rpc type=tandem 11078. 11773 /rnt tyme=tandem	11446. 11306. /rpt type=tandem	1191 <u>6</u> . 11963 /rpt type=tandem	1206112685 /rpt_type=tandem	1274413089 /rpt_type=tandem
TITLE Direct (JOURNAL Submitte Univers SOURCE	repeat_region repeat_region	repeat_region	repeat_region	repeat_region repeat_region	repeat_region repeat_region	repeat_region	repeat_region repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region

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/note="GeneilD exon scores (in order of location ranges):
1.46, 2.66, -0.45 - GSCJ_ID dd_03180"

/codon_start=1
/product="hypothetical protein"
/protein_id="AAA052635.1"
/protein_id="AAA052635.1"
/protein_id="AAA052635.1"
/translation="WILIGILSSISNVKSISKSNNLSSLSNSLSSLQSMNSIERRGGISISNPGFLGGIGRNPGESMVCDSG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTILGSISSIGNVKLISKSNNLSSLSNSSSLQSMNSIQCGGGC
GNGGLLGGVGGLVGGVLVGTGVLVGSVLHGVGSILTGGSNNCGCN"
complement(join(3484. .3740,3824. .3836))
/note="GeneID exon scores (in order of location ranges):
25.27, 0.79 - GSCJ_ID dd_01274"
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GNGGLLGAVGGLVGGVLTGTGVIVGSVLHGVGSILTGGPNNCGCN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(1507. .1763,1872. .1884))
/note="GeneID exon scores (in order of location ranges):
19.50, 3.22 - GSCJ_ID dd_01276"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(4219. .4228,4659. .4915)
note="GeneID exon scores (in order of location ranges):
7.18, 24.38 - GSCJ_ID dd_03039"
                                  Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular
                                                           Biotechnology, Beutenberstr. 11, Jena 07745, Germany On or before Mar 4, 2003 this sequence version replaced gi:19920063, gi:20066239.
CDS predictions from GeneID do not necessarily reflect true Further Information is available from IMB Jena, Department o Genome Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="3323568-3470138"
complement(join(<63. .86,436. .603,692. .704))
                                                                                                                                                                                                                                                                                              and the Univerity Colonge, Institute for Biochemistry (http://www.uni-koeln.de/dictyostelium/project.shtml Funding
                                                                                                                                                                                                                                                                                                                                                                                                           : Deutsche Forschungsgemeinschaft (DFG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                      (http://genome.imb-jena.de/dictyostelium/)
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/protein_id="AAO52595.1"
/db_xref="G1:28830121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein"
/protein_id="AAO52593.1"
/db_xref="G1:28830119"
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/protein_id="AAO52594.1"
/db_xref="G1:28830120"
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/protein_id="AAM33147.2"
/db_xref="G1:28830122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              db_xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .146570
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      Direct Submission
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TITLE
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                                                                                                                                                             SPENDANKE GTPHYPRINDPOTATION TO STAND T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum chromosome 2 map 3323568-3470138 strain AX4, complete sequence.
ACI17072 ACI16964
ACI17072.2 GI:28830117
                                  GSSEEEKĞEVVKDTEAAVPKQDTQPKEEVNPCKIVEELFKSTKNFEDACGLKYGKNYG
WKCVPTTSDKGSEPTARGHSHVARSADGAPSGDKDGAICIPPRRRKLYLHKIEGVDTT
DDKSLRKWFIESAAVETFFLWDRYKKLNTPQSGSPLLGGGLPGVGVENGDDENNPEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IEVVLEPSGNNTTASGNNTTASGKNTPSDTQNDIPSGDTPNNKLTDNEWNTLKDEFIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NMLQSEQPKDVPNDYSSGDIPFNTQPSTLYFDNNQEKPFITSIHDRDLYTGEEYNYNV
NMSTNSMDDIPISGKNDVYSGIDLINDTLSGNHNVDIYDELLKRKENELFGTKHHTKH
                                                                                                                                    LQKGEIPDGFLRQMFYTLGDYRDILFSGDKDKKNGYSDIVSGDNVIKERENTIKEKIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNTYNVAKPARDDPLHNQLNLFHTWLDRHRNMCEKWKNDNERLAKLKEEWENDTSTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 CTTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTCTTTGCTAATCAATAAATTATC 128
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1 (bases 1 to 146570)
Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P.,
Lehmann, R., Baumgart, C., Parra, G., April, J. F., Guigo, R., Kumpf, K.,
Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            y Match 9.9%; Score 52.4; DB 3; Length 251551; Local Similarity 57.2%; Pred. No. 0.21; hes 95; Conservative 0; Mismatches 71; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 AAAAGAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAG 174
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Dictyostelium discoideum
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Direct Submission
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AC117072/c
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CDS

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/ Codon start=1
// Codon start=1
// Codon start=1
// Product="Genello exon scores (in order of location ranges):
// Codon start=1
// Product="hypothetical protein"
/ Product="hypothetical protein"
/ Product="manages | Protein"
/ Product="manages | Protein"
/ Product="manages | Protein"
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ETKYRLDNTNAEYAKLNKSVAMKKKAGESADEIIAQAEELNQSIIKLKAEVSEVELLL
RKKLRPIGNIVHESVPIDNNEDNNQIIKTWGECKTSEGLLHHHBLLEMIDGYDPERGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVSCHRCYPLKGIGVLLNQAIINFALMHMTKRGSVPLQTPFFMNKDVMAKTAQLEQPD
DELYKVTGDNEEKYLIATSEQPISAPHQDEWIEEKDLPKKYVGYSTCFRKEAGSHGRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Original source text: D.discoideum (strain B or Ax3) DNA, clone DD109 DA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Organization of a gene family developmentally regulated during Dictyostellum discoideum spore germination J. Mol. Biol. 205 (1), 63-69 (1989)
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1 (bases 1 to 958)
Giorda, R., Ohmachi, T. and Ennis, H.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Pred. No. 0.49;
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/note="109 gene 2 protein"
/codon_start=1
complement (15517. .15972)
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433. .816
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Location/Qualifiers
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Dictyostelium discoideum
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Similarity 53.0%;
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IKAILSILKSSRSMAYPLSGKKQVLVDLLTSIGFVGPINTSPQPQPPPSPTPPGL
FQEELQPHSFLELDLGITVELDNLLGEN"
join(13881. 13926,14100. 14230,14342. 14589,14703. 15129)
/note="Genell exon scores (in order of location ranges):
/codon_start=1
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LSFNNLKSKPFKIYQRATLTPKYPVFLNFKKRENK"
complement (9415. .11361)
/note="GeneID exon scores" (in order of location ranges):
133.26 - GSCJ ID dd_03256"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISRKSFDCSTSNGISEFGGDDGGCGGGCGGDMGNNINISINKRHNSVNSISSNKNINC
LYHDLANDLITYCNDCERMICYQCIVSNDHCGHKFTEISKPFASSLLEKFQKQQFPNLL
LYHDLANDLITYCNDCERMICYQCIVSNDHCGHKFTEISKPFASSLLEKFQKQQFPNLL
WNEBLQNSIKQDCNDVBRQHISENWQVKQHFQKLIESIGSIEKDIIEKLOSTVE
WNKELQNSIKQDQOIYDFETKQHIEINSDGCTV
PLLKRRLEILANNOSSSKIKFKNDLLTFPNMEIPPEIKEKTLNFFKIENVEXKODLKSTVQ
HLMLNKKIQPYNIDYYLCHGEPIPLGFTSVALDSKYSSKSICIQSNKSIDRLLLCNGF
KLSLSERKIPPITMGSIPSVNELHMCGPFSLQLAPFVLDNSITSLSIGEIKYSILDFFI
PSSVKKIRLYSSFNHPIIPQNISESVFTLVLFNIKLALFITSLSIGEIKYSILDFFI
PSSVKKIRLYSSFNHPIIPQNISESVFTLVLFNIKLALFNCTPGFPQ
QIQPFSIENGGKLEKLVLCDIKEKLLKNSIPNSVKKLIFLGFTNDGFEQ
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PQLANNIKOERWQKIKWQVNLSGLIKWKKEFLDSFKESKLSPTVQELCELIINYKMY
PSEKYYLCAVEKMLNVSTLPHLTPEEVIEFNKNQNSGSRLNSSTNTTTTTTTTTTT
PTEKKUNNDDPNLDSFAFSSSFTTSFPSDTTSSTSTSLSTDGEMKDLDVEQQKDDTDNT
ANENESK"
                                                                                                                                                                                                                                                       product="hypothetical protein"
product="hypothetical protein"
protein id="AAO52596.1"
db_xref="GI:28830123"
translation="MTILASISSIGNVKSI8KSNNLSSLSNSSSSLQSMNSIQCGCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="mimilar to Dictyostelium discoideum (Slime mold). CIGB protein (Fragment) " protein id="AAO52598.1" | /db xref="G1:28830125" | /tb xref="G1:288310125" | /trānslation="MMEPINYKNISFNDIKLDSNCNSSSSSSSSSSIGSNRSGSGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'translation="MTLVEYSETLKKSLEEFCKODKKVVTPELNSIIENISKTGITCY
translation="MTILASISSIGNVKSISKSNNVSLSNSSSSLQSMNSIQCGGCGN
                                      GGLLGAVGGLVGGVLTGTGVIVGSVLHGVGSILTGGSNNCGCN"

join(6487. .649),6572. .8682)

/note="Genello exon scores (in order of location ranges):

3.30, 26.87 - GSCJ_ID dd_03141"
                                                                                                                                                                                                                                                                                                                                                                                                                                             NGGLLGAVGGLVGGVLTGTGVIVGSVLHGVGSILTGGSNNCGCN"
join(7061. 7150,7227. 8279,8516. 9178)
/note="GeneID exon scores (in order of location ranges):
-0.28, 67.69, 40.02 - GSCJ_ID dd_03341"
/codon_start=
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/note="GeneID exon scores (in order of location ranges):
18.88, 1.20 - GSCJ_ID dd_02598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="similar to Dictyostelium discoideum (Slime mold). MkpA protein;
/protein id="AdOS2597.1"
/db_xref="G1:28830124"
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protein_id="AAM33150_2"
db_xref="G1:28830126"
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protein id="AAO52599.1"
db xref="G1:28830127"
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AC116988.2 GI:28829381
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    <178. .805
/gene="TUBA"
806. .916
/gene="TUBA"
917. .>1662
/gene="TUBA"
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                                                                                                                                                9.6%;
llarity 53.3%;
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AC116988/c
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QKLALDYGGKKSKLDPCVYPSPQVSTSVVEPYNSVLSTHSLLEHTDVSFMLDNEAINI
CKNSLDIEKPYTNIARLIAQYISSIVVEPYNSVLSTHSLLEHTDVSFMLDNEAINI
CKNSLDIEKPYTNIARLIAQYISSITSSIARPGQIALDINDIQYNIVPFPRLHFYL
CSYAPVISREKAHHETITVDNITSAVFSEKNIMAKCQPNLGKYMACCLMYRGDIVPKE
AGKAVQNIRSEKSRNVSFVDNSPTGFKGINNQAPVSTKDSEMAEVKKSVCMLSNTTA
ISQVFSRINHKFDLMFVKRAFVHWYVGEGMEEGEFABARDDLLALEKDYSSVSASTEG
EEQEEEY"
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complete cds.
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EDAANNYARGHYTVGKEL I DVCVDR I RRLADQCDGLQGFLVFHSVGGGTGSGFGSLLL.
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                                                                                                                                                                                            47 TGATTTTGCTTCCTTCTTTATGTTTTATTTCCCAAATTTTTCTTAAGCAAATATTT 106
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The highly divergent alpha- and beta-tubulins from Dictyostelium discoideum are encoded by single genes
J. Cell. Sci. 105 (Pt 4), 903-911 (1993)
                                                                                                                                                                                                                                                                                         164 TTTTATTTATGATGATATTAATTAAATATATAAAATGTACATTTACCAACTGAAATTAAG
                                                                                                                                                                                                                                                                                                                        AAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTCTAAG
                                                                                                                                                                 Gaps
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: Clontech) DNA.
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                                                                                                                                  Score 50.6; DB 3; Length 958; Pred. No. 0.67;
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1 (bases 1 to 2255)
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tubulin (TUBA) gene,
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/gene="TUBA"
join(178. .805,917. .1662)
/gene="TUBA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="alpha tubulin"
/protein_id="AAC37343.1"
/db_xref="G1:290059"
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Dictyostelium discoideum alpha t
L13999
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/tissue_lib="Clontech"
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alpha-tubulin.
Dictyostelium discoideum
Dictyostelium discoideum
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                                                                                                                                  9.68;
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Best Local Similarity 53.3
Matches 104; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC116988 331039 bp DNA linear INV 12-MAR-2003
Dictyostelium discoideum chromosome 2 map 6445720-6776760 strain
                                                                                                                                                                                                                                                                                                                                                                  107 CTTTGCTAATCAATAAATTATCAAAAGAAAAAAAAACTGAAAGCAACGCTTGAAAAAAGG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 AAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTTCTAAG 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 331039)
Glockner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P.,
Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K.,
Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence and analysis of chromosome 2 of Dictyostelium discoideum Nature 418 (6893), 79-85 (2002)
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Submitted (04-MAR-2003) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
4 (bases 1 to 31039)
                                                                                                                                                                                                                                  47 IGATITIGCTICCTICTITATACTITITATITIATICCCAAATITITICTIAAGCAAATATIT
                                                                                                                                                                Gaps
                                                                                                                                                                ..
                                                                                             Length 2255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 331039)
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and the Univerity Colonge, Institute for Biochemistry
(http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                Indels
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                                                                                                                                                            90;
                                                                                             DB 3;
                                                                                      Score 50.6; DB Pred. No. 0.65; 1; Mismatches
825
   D
283
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Dictyostelium discoideum
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|oin(20299. .20406,20551. .20660,20960. .21569,21708. .21828,
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/db_xref="G1:28829386"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (join(13231. .14884,15364. .15368))
intea=(geneid exon scores (in order of location ranges):
104.49, -7.13 - GSCJ_ID dd_02788"
| codon start=1 | protein are protein are protein id="Apochetical protein" |
| protein id="Apoc
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DESNNSFKIAMDLANDRNIKGTLIYFGPGGGHLHGLQDDDHNDENSNNEKLDWIGIY
APTDDIVQISPPLALKHDSSGSIMOSNEHIGINLNPAPDRPNNQNKKNGSPKGTILYE
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TFSKLSNSNLLQQYWGLAKGISMKNSTIFKWVKSNLLRKKDDAITIAEEDLYTDDSIS
KNLFRLNYLLIQCKTILNGIVFNENNTIINSPNNETLLKKEKEIPSIFIDKQSKDYQFL
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join (17515, .17664,18062. .19743)
/note="GeneID exon scores (in order of location ranges):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LKDSKEFYFGDI VLFGDQTLNPNI LDTNI LTF ITNRTSMEPEKKKVSDQL I JAKNLLD
QSPSCSCLVSRNGKI IRKI GAFYBELLGLEIGEN ISSVBKASDISTI LKQVOFBNNL
STETTITKKGGEKYPAEVPYKEISOLHSNS I GIMI I VRDI TODI BLKERNI BLQKKSE
LEGYRNQELMEBALDLALTAKI KSGPISTSHEI RTPLNGI I TMGGMLLSTSPLNTEG
HDIARTI FGSSBLLLSITSDILDFSKI EASKLELEM TEPDFIGCLEGIGKTI GVSI TH
KPI BIARTINGSSBLLIGDPNRLI QIMLNMGTNAVYTDRGHI VFRI SVI SREQNRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGSACTSLACIAIAKERGAHTIVTSRNEKKKOOILDYGADYFVSLDTBDIVKRTFEIT
NGKCANIIYDSVGGQSAQKLFESSSQFGKIVPYGNMNHSEPTPLPILIGLKNYLTIKV
LNTNEYLYQPEPNKKAIEFLNSNFHHPKSIVGKEFIGIDSLVDALKYLETGDLFGKVV
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/product="similar to mitochondrial carrier protein family, protein id= Atig14560.1 [Arabidopsis thalians]"
/protein id= Ab051956.1 [Arabidopsis thalians]"
/db_xref="G1:28829388"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="mnssdpkkspkestennsntyrpsktlmtykslkngnnlansli
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bgpkslwkgnganlvkvspnsgirpltyefckkhfldnssnhpssssiengidgngvg
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HSFPKIHKDEGVKGLYKGLGTSIASIVPWVSISFATYEGFKIICKKMILNYQISSSSL
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Likgaalmaegisgpp"
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LLMCKVFNSKCAGISVLNKDGLFDTIAFCSSTQELENFSYSLKKISKNITYYDYMEIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_gtart=1
/codon_gtart=1
join(24256..24266,24388..24538,24623..24750,24902..27
/note="Generon scores" (in order of location ranges):
-2.62, 6.90, 11.20, 259.32 - GSCJ_ID dd_01978"
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/db_xref="C1:28829389"
                                                                                                                                                                                                                                         /note="GeneID exon scores (in order of location ranges): 87.29 - GSCJ ID dd_02787" /codon start=1 /product="similar to Burkholderia sp. DBT1. Putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="GeneID exon scores (in order of location ranges): 9.06, -2.15, 55.50, 6.70, 58.02 - GSCJ_ID dd_01980"
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98.40, 31.82 - GSCJ_ID dd_02784"
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KIPDKSTTAKDYNGARSVPBELITATINHAKTRVVKKARSNUSHSPSSRYDUSKYGVTG
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KVNTNGYGASIYLGSDITLRYESVVDSESNSYLEFETVVDLYKDSITKFTISNLLSN
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KTRIKTRIKTPENFENFORMENENFENFORMENENFENFORMENFENF
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complement (join(2345. 33098,3189. 3526))
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TEFIAAAAEVRKELVKKAQTVVDSLPEELRTEGSYYVKVMKTIAEKSIDFVTTEIARI
YKLVSGSMSGKKADEFAKKLMILESFKEK"
join(5792. .6179, 6292. .6567, 6659. .6881,7332. .7363,
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/note="GeneID exon scores (in order of location ranges):
14.11, 5.65, 10.80, 0.73, 45.28, 141.12 - GSCJ_ID
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stranslation="MAINLLKFFIIYFCFVLINFCNCQTLKITDISNPKNYKVYPQY
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YLDYNLDISNSKINYYPNETTHVVSFFGLGCSTVYSVTINKTSNDYEPYLYVDDGNSKN
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MSASFESSKTKEICSLKDFGETSNGDNSNYFKIQINDHSLYGRFIKRAIIDSKISTIE
NVLLDSKANSIQTASSSQSYIGITIPNYQKSIIIDPDFSVLIDSKSTSKNDENSVCTP
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TCLGEPICGGPKQGFCSSKGCVCYQPWIGNDCNAQVVIIPQPSTNTSQPSTEIPIIDN
NNNQQPSGINYLYKSLISIVSIRELDFNGNQINLYPFDRWIFTQINQNKSQYFTSIKN
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//note="GeneID exon scores (in order of location ranges):
1.76, 12.26 - GSCJ_ID dd_02786"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="GeneID exon scores (in order of location ranges):
10.46, 12.19 - GSCJ_ID dd_02783"
/codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1427))
                                                   Deutsche Forschungsgemeinschaft (DFG).
Location/Qualifiers
                                                                                                                                                                                                                            'organism="Dictyostelium discoideum"
"mol_type="genomic DNA"
strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="6445720-6776760"
complement (join(912. .1165,1280.
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/protein_id="AA051923.1"
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                                                                                                                                                                                     .331039
Funding
                                                                Agency
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CDS

SGS

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DNA linear HTG 03-MAY-2003
*** SEQUENCING IN PROGRESS ***, 6
                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostel; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (Dases 1 to 16744)
                                                                                                                                                                                                                                                                                                                                         clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                               Submitted (02-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 16244; sum-of-contigs
Insert size: 173147; 3.5% error; sgarose-fp
Quality coverage: 1.49x in Q20 bases; sum-of-contigs Quality
coverage: 0.60x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                           On May 3, 2003 this sequence version replaced gi:30142548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14139: contig of 2805 bp in length 14239: gap of 100 bp 16744: contig of 2505 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of 100 bp
contig of 3262 bp in length
gap of 100 bp
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gap of 100 bp
contig of 2262 bp in length
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of 2805 bp in length
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Chemistry: Dye-terminator; 100% of reads
Consensus quality: 11041 bases at least Q40
Consensus quality: 12485 bases at least Q30
Consensus quality: 12485 bases at least Q30
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/note="assembly_fragment:00455"
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/note="assembly_fragment:00565"
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Center: Wellcome Trust Sanger Institute
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Danio rerio clone CH211-117012,
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/db_xref="taxon:7955"
/clone="CH211-117012"
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/organism="Danio rerio"
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Danio rerio (zebrafish)
Danio rerio
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AUTHORS
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of PFMALBP1 from base 100001 (AL844507 Plasmodium falciparum 3D7
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DQIFEESNIILVKESTVKKFFELVQEYKINGDVNKIDLKNLDPELLPFFDSSLICIIV
FHRFMDNLDIFLKYVKDFIEFYKKKIVVALGINHKNFKNLPKRRDFLIFKKPISSTNL
                                                       IKVSNMARKI I PKSSSSSNLI QTI SQI DNQQQQQQQQQQQQQQQQQQQQQQQQQQQ
VTI SPHSDSSEKKTTPKKDRGKYDFNI SPLRI DRFGTESTSSPKI KLYSDTSSDSGES
DEFEFSENLRELKSDGELVVLKNQPYREQRLSNI QLINDPI VTPPTPKANSEVVSTKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 AAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTCTAAAG 226
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                                                                                                                                                                                                                                                            Length 331039;
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0.52;
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Pred. No. 0.52;
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Best Local Similarity 53.2%;
Matches 107; Conservative
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Best Local Similarity
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Continuation (2 of 14)
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PFMALSP100
PFMALSP101
PFMALSP102
PFMALSP103
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SOURCE
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TITLE
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AUTHORS
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Lardy, B., Klein, G. and Bof, M.
Direct Submission
Submitted (17-JAN-2003) Departement Reponse et Dynamique
Cellulaires (UMRS092 CNRS), CEA-Grenoble, 17 rue des Martyrs, 38054
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| Jab.xxef="G1:290281300"
| Lennslation="MSKFKLGAMAAMIGMAACWCLIAGGIMGIWYERRYIAIYSICVG
| CYLYPLLYPLSPLGPLKAIFHQYYVAAALMAGLSVLCYFLVPTWLAAMVMDISAVVFL
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Dictyostelium discoideum p22-like superoxide-generating NADPH
oxidase light subunit gene, complete cds.
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                                                                                                                                                                                                                                                                                          4634 TTTTGTTTCTTCAATAFTTACTAAAAGTTATTATATTAACATATTTACTTACAATAATAAT 4693
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/mol Lype="genomic DNA"
/db xref="texon:44689"
/db xref="texon:44689"
/join(1. 122,284. .>518)
/join(1. 122,284. .518)
/codon_start=1
/product="p2-1ike superoxide-generating NADPH oxidase
light subunit"
/join(1. 122,284. .518)
/codon_start=1
/product="p2-1ike superoxide-generating NADPH oxidase
light subunit"
                                                                                                                                                                                                                                                      61 TCTTTATACTTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAAT 120
                                                                                                                                                                                                                                                                                                                            121 AAATTATCAAAAGAAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTAT 180
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Dictyostelium discoideum
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (Bases 1 to 518)
Lardy, B., Klein, G. and Bof, M.
Dictyostelium discoideum superoxide-generating NADPH oxidases Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                     181 CGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTCTAAGTCC 229
                                                                                                        Length 16744;
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                                                     534 others
                                                                                                        Score 49.8; DB 2; Length 1
Pred. No. 0.89;
1; Mismatches 103; Indels
       14240. .16744
| 14240. .16744
| /note="assembly fragment:00601"
| 2801 c 3068 g 5010 t
/note="assembly_fragment:00571"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
9.4%; Score 49.6; DE
Best Local Similarity 55.1%; Pred. No. 1.2;
Matches 97; Conservative 0; Mismatches
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Location/Qualifiers
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                                                                                                        9.48;
                                                                                                                                          Matches 123; Conservative
                                                                                                                           Similarity
                                                   5331 а
                  misc_feature
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DEFINITION
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ORIGIN
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AUTHORS
TITLE
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AUTHORS
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JOURNAL
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KEYWORDS
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Gaps

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79; Indels

82

26 ATTTATATGCTGATTTATGGCTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAA

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AC116982 256879 bp DNA linear INV 12-MAR-2003 Dictyostelium discoideum chromosome 2 map 3622643-3879522 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Mycetozoa; Dictyosteliida, Dictyostelium.

1 (bases 1 to 256879)

1 (bases 2 to 256879)

2 (beckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e genea.
of
277 AFTITIALITITIALITITIALITITITALITITITALITITITALITITIALITITITALITITIT 218
                                                                                                              86 ATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAAACTG 145
                                                                                                                                                                                217 ATTTTTTTTTTAAATAAGTATTTAATAAATTTTAAAATTTTCAAAATATATAAA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="GeneID exon scores (in order of location ranges): 145.41 - GSCJ_ID dd_03231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence and analysis of chromosome 2 of Dictyostelium discoideum
Nature 418 (6893), 79–85 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (join(2498. .3048,3100. .4441,5088. .5120))
/note="GeneID exon scores (in order of location ranges):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany On or before Mar 4, 2003 this sequence version replaced gi:20042944, gi:19569856, gi:19682956, gi:20042945, cos predictions from GeneiD do not necessarily reflect true gent Further Information is available from IMB Jena, Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 256879)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (04-MAR-2003) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
4 (bases 1 to 256879)
                                                                                                                                                                                                                                                                                                                        157 AATATAAATCTTAATAATAATAAAAATATAATTACATTGAATAGATTGCTATATAT 102
                                                                                                                                                                                                                                                      146 AAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Blochemistry I
(http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Dictyostelium Genome Sequencing Consortium 2 (bases 1 to 256879)
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Location/Qualifiers
1. .256879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AX4, complete sequence.
AC116982 AC116981 AC115574 AC115677
AC116982.2 GI:28828986
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/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="3622643-3879522"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:44689"
/chromosome="2"
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Dictyostelium discoideum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baumgart, C.
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complement(join(18157. .19271,19330. .20271,20399. .20510))
/note="GeneID exon scores (in order of location ranges):
62.84, 35.15, -1.47 - GSCJ_ID dd_03265"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (join(21408. .23107,23187. .23546,23618. .23786))
/note="GeneID exon scores (in order of location ranges):
156.00, 19.78, 12.12 - GSCJ_ID dd_01499"
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NSLSKFKNNSNNINTTVNKYKRWSESKRIYLKCPPSAMDVNPEKKFKFSISILHKENK
DLFESLSLHMLSNLLLRGSNTPMYQALLESGLVLDYSPNTGFDDGLLESSFSVGGIGI
KKEDLEKVEKVIIELLEKSSRDGFASDYIESILHQYEFAQKOVSASFGLKJVGSLSSN
WIHGGDPVDPLFLNEAIAKLRKELEKGGFFETKIKKLILNNPHRLYITMENDENIQKEE
                                                                                                                                                                                                                                                                                                     QEKELQKLERIKSELTPEQTKEIIEVAKDLQPRQNQIQDVSYLPKINICDIEKQQSKI
DHIDTKLSWTNGDGYPLRILDLPTNGISYPRSTIDISSMDPKLKPYVPIFCSLIDEMG
BAEPDHKQDTPEINLHIGKPSYSPLITMGHSDLDYTQERIYKTKGAALMNNLLKMFSLL
QKILLENKWNNPDLLKNLLANQKQASITEGIPSSGLSYAKILSSKFSRAAQLSEQWSG
LSQYRLLINETYSSNIDINSLINKCLAINEFIDRSLMKCLITTEKENISNLENNLSNPL
KPFSNKNTPIIIVNSLDNANEEIINSSKLNFFPIPATISNLENDLSDRY
                                                               VIKIREVPERQFKTYQFEHIETGÄKYLHIDCEDTNNVFSVTFKTIPKDSTGVAHILEH
TTLCGSKKYPVRDPFFNMLKRSLNTYMNAWTAPDHTSYPFGTQDPKDYYNLLSVYLDA
TFPPNLSEQDFRQEGHRLEFEQMENPQSPLKFKGIVPNEMKGALSDPSSFYAEISQQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILTKVLSEFLHKEIREKGGAYGGSSVDSGVISFYSYRDPNLIKTLDAFDGSIGWSLN
NKTLENIRANDLSIFSDFSPSRSYRGYGFMANDITNEMKGTRRNNLLSITKPKLE
BIATKKLFRNGNNYTTVLGSKGNOGELNKFTRNNINU*
complement (join (15763. .15963,16072. .16305))
//ncte="Geneld exon scores" (in order of location ranges):
1.81, 0.51 - GSCJ_ID dd_01491"
//codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MYLHLERNCKGINSLKSIPRHYMLLDGFKEKLSEGILPEGVQNL
FLGDIKQDLTIDSIPNSVKAVYLLNGFNQKKTCRNGISTNKLTCGIIPEGVKTLEICD
IKQQLTIDSIPKYVSEIIIQRKIKQTIIPFQIPKNITLKYAD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /trānslation="MISKESENFNNTKCIIHTKKDLMVLCLDCNFIPCCIECISINNK
HHGHKFNQIDIOGSTREINLLANNFKDNIYPKIIDRIGNDQFILNESNRTFNKTQLAYN
NNNDIVTKEFKKIHDIISKIELDIKKQLTFTENNQLINFTLANSLANDIEILSPIIN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNTIIDKINDFIKKKONPKNYSIDGNFEIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKCNFIIESEENNLIFKFLSRKYYIYSENHSPLKNYNNDKDGIAFKNNCKGITSLKSI
BLNWALLLASPREKLEBGILEFKGYHRLFLGDIKQELTINSIPSSYKSYYLLDGFWQKLT
AGILPDGYKNLLLAGIKQDLAISIPNSKEFYYLLANGFNRKITAGILPEGVPEFLEGD
IKQDLTIHSIPSSVKFVYLLDGFNQKLTAGILPEGVNFLSLGDIKLDLTIDSIPKSVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ILPEGVENLFLGDIKQELTIDSIPKSVKYVNLLDGFNQKLTAGIIPEGVKILEICDIK
QLTIDSIPKSVCEIIIPMKQKQTIIPPQIPKNITLKYLDN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (16692. .17381)
/note="GeneID exon scores" (in order of location ranges):
27.91 - GSCJ_ID dd_03236"
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/protein id="AAOS1566"
/db_xref="G1:28828991"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="similar to Dictyostelium discoideum (Slime mold). CIGB protein (Fragment)" /protein_id="AAO51567.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="similar to Dictyostelium discoideum (Slime mold). CIGB protein (Fragment)"
//protein id="AAO515681"
/db_xref="d1:28828993"
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Pred. No. 0.97;
0; Mismatches 96; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db xref="GI:28828992"
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Best Local Similarity 52.7
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
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PIFETKLYPQILFRFMKSSDVSKSRYISFISKLILKNILINPIVLYFLLIFYDDIELID
BLISLSTYRSFRYSIDSNSNSNSNSNSNSRYFKTNILKLILKREINNEREINNERFREDPDIKRYI
RSNEMLEFCFTNFRIILLHPFKFKNILTTWYKMDRTDLIETFRNJIKT (OLNDKYNIEND
LILPTIINSGFSITTHSPERKAFTISKLKETRKNFWISNLDEKLLLESLUY
KVNSKILNLDYQLECIKLIIEHTTEQYNPLSIWOTETH.FNSTENDLFILKASYINKO
FLYMLFTNHKVPIPSTKISLALLYLSNOIDQPLIEFSHMLINGSYPQLDIFFETIGKN
SDYKLLGKLIDTFNNFTKSQOSLPKTFNEEKKRLLSLCFFKASVDGNIIIFFKFLLEN
YDNILFPKNSKLPEESFLETDESFQRYVAKAIEKDNHQLFEFFFQNLGYQSILIEFLEY
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/note="GeneID exon scores (in order of location ranges):
207.84, 62.69, 6.20 - GSCJ_ID dd_01492"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MSDNTEILFWKDSIFPKDVLNIDLEILIGLCIIINIPFLKNIK
SSSSPPILTIEEINEIKNKYSEKDLKSNIINLEYDDFNLKKLIKFYDSVRFDIDYNP
FRFLKFDDEGDSNEEINSHANKIYENILTAYQNQPSIPSLEYCNSRLLEKTINDFGTL
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QMPSCTGINKDYILNYNSLVLNNQFSYAQPIINFLTISAKKDMITINGNNFGNSEKVI
QVYYNDVNITSKIQLLNNNQFQIRNNDSFNNGPIEMVVDENNLLSGFNSTLPPIVKKV
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VSVYIGPNLVLSNVILNHSDPNVTKINQVRNDKDGFSIKLSGIGFTDSMDASIVLPNG
SRRAIKCKLQCIANLESTNKINISNGTGFYLCTSKAIIDQDSIGLKMIFNSKLIEFDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(8607. .11368,11918. .11930))
/note="GeneID exon scores (in order of location ranges):
185.43, -3.14 - GSCJ_ID dd_01494"
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/protein.id="AAM44360.2"
/db_xref="GI:28828990"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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mold). LagC2"
- GSCJ_ID dd_01255"
                                                        /product="hypothetical protein"
/protein_id="AAM44355.2"
/db_xref="G1:28828987"
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      -0.12
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5707
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Dictyostelium discoideum Ddp2 plasmid DNA containing gene essential
for replication.
                                                                                                                                   72 TTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAATTATCAAA 131
                                                                                                                                                                                                                                                                                                                                                                                                  District; plasmid: passid bdp2; rep gene.
Dictyostellum discoldeum
Dictyostellum discoldeum
Eutryostellum discoldeum
Eukaryota; Mycetczoa; Dictyostellida; Dictyostellum.

1 (bases 1 to 5852)
Sade, M. B., Chang, A.C. and Williams, K.L.
The sequence and organization of Ddp2, a high-copy-number nuclear plasmid of Dictyostellum discoldeum
Plasmid 24 (3), 195-207 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct. Submission
Submitted (24-JAN-1990) Slade M.B., School of Biological Sciences,
Racquarie University, Sydney NSW 2109, Australia
Location/Qualifiers
1. 5852
/organism="Dictypestelium discoideum"
/mol type="genomic DNA"
/strain="WS3808"
                                                                                                5766 irriaarratratrirgiarrirrirriararararrirrigirgirgirrirrirgi
                                                                  Gapa
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Identification of the origin of replication of the eukaryote
Dictyostelium discondeum nuclear plasmid Ddp2
Plasmid 24 (3), 208-217 (1990)
                                  ;
 9.3%; Score 49.2; DB 3; Length 5850; 57.0%; Pred. No. 1.3; tive 0; Mismatches 68; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1100. .1109
/note="palindromic sequence tgtcatgaca"
1137. .1638
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note="palindromic sequence tgtcatgaca"
285. 1294
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2172. .2181
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/cell_line="HU2362"
572._.1072
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/note="palindromic
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                 l Similarity 57.0
90; Conservative
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DDP2PLAS/c
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5850 bp DNA linear INV 27-APR-1993
Dictyostelium discoideum plasmid Ddp2 trans-acting factor gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="trans-acting factor"
|protein id="AAA3191.1"
|db_xref="GI:167728"
|/translation="MDELISWDRFFKFFVILLEEFKGCKRNDVRLSVDYDILSGIYSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source text: Dictyostelium discoideum (strain WS380B) DNA.
Location/Qualifiers
                                                                63 ITTATACTITIATITACCCAAATITITCTTAAGCAAATATITCTTTGCTAATCAATAA 122
                                                                                                                               ATTATCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAAGGAAAGTTAGCCCTATCG 182
 62
                                                                                                                                                                                                                                                                                                                                                                                                  trans-acting factor.
Dictyostelium discoideum
Dictyostelium discoideum
Dictyostelium discoideum
Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.

(Dases 1 to 5850)
Leiting, B., Lindner, I.J. and Noegel, A.A.
The extrachronosomal replication of Dictyostelium plasmid Ddp2
requires a cis-acting element and a plasmid-encoded trans-acting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (5073. .5113)
/note="putative VECTOR sequence Cloning vector pEMBL 8
minus (pEMBLBM) (X04996); putative"
a 646 c 706 g 2198 t
1795. .1829
/note="putative VECTOR sequence Bacteriophage lambda
(J02459); putative"
2372. .5041
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Dictyostelium discoideum"
/mol_type="genomic DNA"
/strain="WS3808"
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Plasmid Ddp2
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DDIDDP2/c
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                                                                                                                                                                                     /db_xref="SPTEMBL:023913"
/db_xref="SPTEMBL:023913"
/translation="MDELISMDRFRKFYILLEBFKGCKRNDVRLSVDYDILSGIYSP
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IRVSDVDQAILIFDHFSRISKQVPFROIIGYRTFEKSISSEYKISDGRAAGVSWFN
LVSKISTYCKNHPLFAENPTYKHVDFISMLSLVHGIIVDSQNEDENNVSAMYSLNFFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT 07-JUL-1994
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/gene="REP gene from a recombinant Ddp-2 like plasmid in
Dictyostelium spp"
2378. 5041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2378. .5041
/gene="REP gene from a recombinant Ddp-2 like plasmid in
Dictyostelium spp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMPROVED PLASMID VECTORS FOR CELLULAR SLIME MOULDS OF THE GENUS DICTYOSTELLUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 5852;
                                                                   'note="essential for plasmid replication"
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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'note="palindromic sequence tggcatgaca"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 AGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAA 169
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1. .5852
/organism="synthetic construct"
/mol_type="genomic DNA"
/db xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                              MGLEDEDEDEDEDEDEDEDEDEDEDEDEDGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
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Pred. No. 1.3;
0; Mismatches
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Dictoselium plasmid Ddp2 REp gene.
                                                                             /protein_id="CAA35843.1"
/db_xref="GI:7308"
/db_xref="GI:7308"
                                                                                                                                                                                                                                                                                                                                                           709 g
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Best Local Similarity 57.0%;
Matches 90; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 5852)
                                        2378. .5041
/gene="rep"
               378. .5041
/gene="rep"
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DLEKSII PGAVOSKUTTNRTRGSRSNBNLNNPTTTTTTTTTTTTTAP I TTRSKRKSDD
SVQEQSSRQPKTSRKSGSLKDVRINNI SVDSSSSESDVIMSVSNRLKCYLLEAVVNKG
BIGLEVVRKJKDLQDKNYSTGLLENI FNHKKSERVITLSSSFPEIASKINVDEVVRS
BLSIDVLESAKRLTFEKVNINI I PTNNFKGFEPFLWPI VNGI JASTSVFVSPNNYSSG
SFANVBSALKLIHLGI SLGNINGFLSIRSI TFDTFKSI TKDLI PMSKRMLDLEGGFFK
IRDAMNNSNKKSKVQDSDI SGIDTEDTKLI SFVHEFINDNLYLKLSKEEDGLMLVDFP
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/db_xref="G1:583619"
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/translation="MDELISWDRFFKFVILLEBFKGCKRNDVRLSVDYDILSGIYSP
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RYSDVDQAILIFDHFSRISDKQVFRKDIIPGYRTFFKSISSERKISGGRAAGVSWFN
LVSKISTYCKNHPLFAENPTYKHVDFISMLSLVHGIIVDSQNEDENNVSAMYSLNPFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NELKKKYSLMVSDFRNVPKVTPKFIPSEFKRFTITFTNNSYNANRVFAFDDISSGIS
INTVKNIHARGQRNFBIYETLLGSTRIIRAFYCAPCLIQINNSKFAFNGIDDOSVNH
QIASLEIKNLSYLFPLDIKYRGSTVGTIKGGSTRATIINSEFTFSISCLDIRESASLI
SKTKLSQLPFPAPDERXNKGTVILKVLDQCDELTRTFLANYKLANKKISTIENYLYNNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5707 АТАТТТСТАТТТТТТТТТТТАТАДАДТТААТТААТТТААТТТТААТТААТТААТТААТТАААТТАТ
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Dictyostelium discoideum chromosome 2 map 5515173-5817331 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 TTATTTATTCCCAAATTTTCTTAAGCAAATATTTCTTTGCTAATCAATAATTATCAAA 131
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Nature 418 (6893), 79-85 (2002)
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Baumgart, C.
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Best Local Similarity 57.0%; Pred. No. 1.3;
Matches 90; Conservative 0; Mismatches
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Dictyostelium discoideum
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AC116977
AC116977.2 GI:28828573
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                                                                                                                                                                                              Direct Submission
Submitted (127-MAR-2003) Genome Analysis, Institute of Molecular
Submitted (27-MAR-2003) Genome Analysis, Institute of Molecular
Submitted (127-MAR-2003) Genome Analysis, Institute of Molecular
On Mar 4, 2003 this sequence version replaced gi:20042932.
CDS predictions from GeneID do not necessarily reflect true genes.
Further Information is available from IMB Jena, Department of
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Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 5 (bases 1 to 302156)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Blochemistry I
(http://www.uni-koeln.de/dictyostelium/project.shtml
Funding
Agency : Deutsche Forschungsgemeinschaft (DFG).
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Location/Qualifiers
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                                                                                                                                                   AUTHORS
TITLE
JOURNAL
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                                                                                                    REFERENCE
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CDS

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L. Nature, 419 (6906), 527-531 (2002)
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                                                                                                                                                                                                                                                             PPA929353 343050 bp DNA linear INV 29-JAN-2003
Plasmodium falciparum strain 3D7, chromosome 5, segment 3/4.
AL929353 AL844504
AL929353.1 GI:23504644
  Submitted (20-SEP-2002) P.falciparum Genome Sequencing Consortium, The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxcon, Cambridge CB10 18A, UK For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
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Similar to Dictyostelium discoideum development protein
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scores: E(): 2.6e-16, 37.267% id in 161 aa"
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Devlin,K., Baker,S., Davies,P., Mungal,K., Berriman,M., Pain,A.,
Hall,N., Bowman,S., Churcher,C., Quail,M. and Barrell,B.
Direct Submission
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                                                                                                     147 AAGCAACGCTTGAAAAAAGGAAA 169
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Plasmodium falciparum 3D7
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                          SLKLKIENDIVLCVGNEIITSSGGKEIMKVCNEKLQLKQSDLKSILAGAESGGESEIL
INSLEQQLLKLIEEYPLPLGPKSIDDIKQLKLADVDPVSTYDHIQSIEKLIPESKCHK
CHRHDHYEQTEKRYQLQYAIRDAKYTASDENLKLMPQFNIRLDILHELGYIDDENTY
TLKGRVYETSTETTENTCEDLVITEILEN FINLEPSEVVSYLSCLIFQEKDAVQPSLTPRE
EEAKQNLIKTARKYTKYBSDKGLDVVPDDKLETTLKFGLMQVYYBWARGTPFNDICTL
TNVLEGSIVRAITRIGETCQEVRNAARVIGDTKLLQKMEEAMRLIKRDIVFTSSLYNN
                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MEIINYLPPAACENCPQHKYCTRCYFQQLQFMSALTIHQKEISQ
PKKRKNTGHDEPNSNFYESDIESDDDBQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ
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SSNIEKEVNDODDDDDNNDDDEIFENEKYTIGLILECKSTLIKQYTNTKVDRVPKIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQQQQQQESESRTVTGIQIEFDDEIEFVH"
complement(join(20381. .22148,22235. .23160,23330. .23685,
24790. .24793))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAT 06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146
                                                                                                                                                                                                                        /norde="Genello exon scores" (in order of location ranges):
41.07 - GSCJ ID dd_02896"
/codon start=1 /product="similar to Involved in global regulation of
rranscription; Snf5p [Saccharomyces cerevisiae]"
/protein id="AAOS1182.1"
/db_xref="G1:28828579"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 AAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAAT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="GeneID exon scores (in order of location ranges):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 TITATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTATTCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schlegel, R., Deeds, J., Berger, A. and Zhao, X. Genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of cervical cancer patent: WO 0.14247-A 2746 14-JUN-2001, Millennium Predictive Medicine, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 302156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48.8; DE
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2746 from Patent WO0142467.
AX187051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ų
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Pred. No. 1.9;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                         complement (18767. .19162)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     611 ]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 54.4%;
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84; Conservative
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Best Local S:
Matches 84
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
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ORIGIN
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AX187051
LOCUS
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VERSION
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AUTHORS
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                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
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cation-transporting Arpase 1 SW.ATX1 PLAFA (004956) (1956 aa) fasta scores: E(): 0, 97.919% id in 1970 aa Large N- and C-terminal extensions In 1970 ab transmembrane helices predicted by TMHMM2.0 at aa 50-72, 286-308, 334-356, 361-380, 708-730, 2173-2195, 2207-2229, 2263-2282, 2302-2324 and 2334-2356"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trānslation="myknipppunikketykvyyyhtnnlihdeyrisyiecykkkk
KKIVTILHYVPCILSLGLLPLILSWPPIPYFRLLHSACTLNECEKVLIITKDGNKYIK
KIKKIKFNHNVCYVMNDVFFSEDQSMSSMYNDKEQNKNNPNYFSRDYTFRDQNIMNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKYSKNELMGKTIKNQVGVDTNIYHMNCDNDYNYDYPCDYNCNNCNDTYHRLEYHNIN
KDNSFNIPPEKNKSYNNISEHIKINYPLLFEALACCHTLSKVNNKIMGDVLEILMFNF
TNCDMLINNNSFIIKEKKKNCSYDFQXIDGDKNIGANDERCHLNNNLVSYNILKRFEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASLCSFRLISQKDVSKILCTSSSKHIKYLTDDNSKYLYRHSLAFQAINYLKIFMNKFR
FASSKKQWNELGKKINNKLKSYPFSLSKLKGSSDDEHKKKHRKIINNRKMLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSRLQRMSVIVKSTYGNNNDDNNDDDNNNDDDNNNDDNNNDDNNNDDNNDDNNNNYYY
NIFCKGSPEKIKELCLKSKIPNNYDEILNKYTKQGMRILSISYKRVKSKNINLLNVKR
                                                                                                                                                                                                                                     /trānslation="MRKVSIKFINSRLYYSRRYLSRNQFYSFFSCNKNEQRPIKSKND
DFLIDESYNNVEFDEYISPSFSFDINIDDDKWKKKEEIEYNKFIEKTKKDSINFSTFF
                                                                                                                                                                                                                                                                              NTQKATKHIKNTSGNSNYEKLQIHNKHIDNNISSNVVTSNNSTPHNVETFYEKENIYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NELMGKTIKNELMGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELMGKYSKNELM
TNIKKELSKIILIDDSNISGFQYPDNFFPIKKWQGDLNDNELLHLIPFFLNLRKLKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Similar to Plasmodium falciparum probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="cation-transporting ATPase 1"
/protein_id="CAD51525.1"
/db_xref="G1:23594647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(7484. .14348,14522. .14859)
/gene="PFE0805w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .14348,14522. .14859)
                                                                                                                                                                     /product="hypothetical protein"
/protein_id="CAD51524.1"
/db_xref="G1:23504646"
                                                                               gene="PPE0800w"
|oin(3549. .6704,6817. .6915)
|gene="PPE0800w"
                                                             oin(3549. .6704,6817. .6915)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               number="3.6.3.-"
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                                                                                                                                                   codon start=1
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YFEKREIQKKYNHNHMSSIFCSPQELDTINVFVTCN"
complement (join(15807. .15912,16021. .16198,16441. .16612))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(15807. .15912,16021. .16198,16441. .16612))
/gene="PPE0810c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Weak similarity to several tRNA pseudouridine synthases, incl. Staphylococcus aureus tRNA pseudouridine synthase a trua TR:BAB45147 (EMBL:AP003164) (267 aa) fasta scores: E(): 0.0011, 30.952% id in 126 aa Signal peptide predicted by SignalP 2.0 HWA (Signal peptide probabilty 0.925, signal anchor probabilty 0.071) with cleavage site probability 0.497 between residues 24 and 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INGIYFIKSKLINKIENKKONTOKKOMKLPCDHNDNVNRMEQQNNSVNVSKDNSSFIFSNR
KKLTNLLLIVNYDGTNYNGMTGLENSSEVYLMALQNYKWKKTERQKOIERKKYSTVO
NNLDECILLIGYKYIHNNNNEHICHSSKYVCONTOWNAHNDYNQNNAHNNGFINNKP
FEFTGVSRTDKGYKKYTCOYITSYEKEPPCOGDMEHIKRSLINSLLINKDINALNKKE
PHDHFNIRFHNSGKIYTYNLDIRNPSQPLERNYAMQLYDDPRFFFLSKKTNKHKKEGT
                                                                                                                                                                                            LKNKYRIVNNGYMLKNDNYVPRHMYNLTDMYRGTOYGCSKKKNKNIYMNNNILKN
KRINRPLEHLLYDKCKRNICHCHYTDIYRKLAIPYRYBINKCKNITYARMKROKSDILISL
KKLPNNSYGWCGGOANDCLALSCADIGISLCNNNSSSICSSFTSNKLCLHSYVHILL
EGRASLVNSYGCHOANDCLALSCADIGISLCNNNSSSICSSFTSNKLCLHSYVHILL
EGRASLVNSYGCHOANDCLALSCADIGISLCNNNSSSICSSFTSNKLCLHSIFWC
WARABEKLSKNIPIGKLFSPPILISIYTOGIIIOLEFWMISULTLAIMNSFLKYP
KEKSDDTYLYKAQWILLYILCSCAPULFMCTSLNIKNEWRKSYFTNIRFITIMSFLLIMSFLLIM
NTCITFPSSEIFLVGWIIDLLKQYLSLITFPPYFRIPLPFFILPFPILFSYSYEKYIIK
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NLSDEKQNCLDCEN I STNH I SSSND PPNDN I CLSNDL PNDN I CLSNDL PNDN I CLSND
LPNDN I CLSNDL PNDN I CLSNDL PNDN I CLSNDL PNDN I SPSNDL PNDN I SPSNDL PN
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HNFECFRGTLKGTEKLRKINTFCTIHFLDVYELKNNLYQFVI QGDRFLYHMIRI I VGT
LVQVGVGLLNVEDVRDALHLCKPLKVKLCAPSQGLCLNKI LLQEPLDKLIGSALISN"
                                                                               TYTSNNIYLSKYKYVHKNYYYPDSCTNLRKKKNSLPYNLKKYIYYEKKKYLQHCLLK
HWYXKVELPRIKDINYSYQMESIKTNPIHELEBEQPAIFSHILLSFYIKNDNNVY
HKNYIYNKYIIYNKYYIYKKYICHKNYIKNYKNHYNYKKNIITHAKSYLLSG
SSKKFLKFPSNIIRHKLKEKKNKKNIKRYKMNYNNTSKGHIILMCTHGFKKVYSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at aa
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YEHRTNDIQPDKLCDILINKDPRNVNIVLTGKAPIPLKKKPYSFHLPYYBECKNIVHY
                           IMKKKHKKIKNI INNHUSULYYHYUI IDTPVKRMNKBYMCPUKLLYKIQQKLLYULH
NLYKKKKYMNYYDI DEVHLIGUNNNNNKNUSKEKKLPLKNKMKHIRKNESUDUITPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MNKFFPLLVCVSLIFFFLKLSINAKKIFKKNIKNKPFILKKSNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 ITTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 probable transmembrane helix predicted by TWHMM2.0 5-24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
/protein_id="CAD51527.1"
/db_xref="G1:23504649"
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="PFE0810c"
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/gene="PFE0815w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="PFE0815w"
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INV 29-JAN-2003

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Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Buckec, C.O., Burrows, C., Chereveach, I., Chillingworth, R., Corton, C., Christodoulou, Z., Clark, L., Clark, R., Corton, C., Croin, A., Davies, R., Davis, P., Dear, P., Dearden, F., Doggett, J., Feltwell, T., Gobble, A., Goodhead, I., Gwilliam, R., Hamlin, N., Hance, Z., Harper, D., Hauser, H., Hornsby, T., Holroyd, S., Harper, D., Hauser, H., Hornsby, T., Holroyd, S., Larken, N., Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larken, N., Line, A., Maddison, M., Mclean, J., Mooney, P., Moule, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A., Rabbinowitech, E., Rajandream, M.A., Rutter, S., Kutherford, K.M., Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R., Squares, S., Stevens, K., Taylor, K., Tivey, A., Unwin, L., Whitchead, S., Woodward, J., Sulston, J. E., Craig, A., Newbold, C. and Barrell, B.G.

L. Nature 419 (6906), 527-531 (2002)
                                                                                                                                  PFWAL13F7
PERMAL13F7
PERMAL13F7
PLOUR Plasmodium falciparum MAL13F7, complete sequence.

AL0134559 AL008974 AL008975 AL008981 AL008983 AL009015 AL010138
AL010143 AL010146 AL010154 AL010157 AL010160 AL010165 AL010169
AL010187 AL010189 AL010208 AL010208 AL010214 AL021885 AL021888
AL139179 AL844502 Z288556 Z98557 Z98558
AL013959, 4 Gil 8052273
S HTG; 405 Ribosomal Protein S3A; acyl transferase; cyclophilin; elongation factor; F84012.11-11ke protein; Hedicase; cyclophilin; protein; histome H2A variant; kinesin-related protein; neactylglucosamine-1-phosphate transferase; protein kinase; R-G77 repeat; R-F81 repeat; repl1; rep20; rifin; RNA-binding protein; stevor; T-complex protein 1 epsilon subunit; telomere; var. Plasmodium falciparum 3D7
Ribaroria: Allondarum 3D7
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Direct Submission
Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 253305)

Bowman, S., Lawson, D., Brabham, D., Brown, D., Chillingworth, T.,
Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T.,
Gentles, S., Gwilliam, R., Hamlih, N., Harris, D., Holroyd, S.,
Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J.,
Moule, S., Mungall, K., Murphy, L., Oliver, K., Quall, M. A.,
Rajandream, M.-A., Rutter, S., Skelton, J., Squares, R., Squares, S.,
Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On or Deficie May 14, 2001 this sequence version replaced gi:2882540, gi:2882541, gi:2882544, gi:22894453, gi:2892564, gi:2892564, gi:2892565, gi:2982565, gi:2982566, gi:2894491, gi:2982569, gi:2894507, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:2894502, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:289402, gi:
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MEDLINE
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MEDLINE
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AUTHORS
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KEYWORDS
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                                                                  138910 AATTATATATTTAAAGAAATAAAATAAATTTATGTCAAATATTTTTGTATTTTGAAAAA 138969
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PkAAPKPBATAPKAAAAKEAKARPBAGTHNGYYKWWGGGSYTDATR FSAAGKVVS
AQIRRRKYALIFFENAAAVKKJIDLFNEKEVLGAKVTVSPAKTSPEKPDPEGSSVVFL
SPIFRNSTTNGQIRELFTGMRVLIRIRTYRQNYAYVYLDSAAAAQKFVKEKNGTEFRGK
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Zhang, J. and Williams, N.
Direct Submission
Submitted (24-AUG-1997) Microbiology, State University of New York at Buffalo, 3435 Main St., Buffalo, NY 14214, USA
Location/Qualifiers
   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF020696 1052 bp mRNA linear INV 21-OCT-195
Trypanosoma brucei RNA binding protein (TBP37) mRNA, complete cds.
AF020696
                                                                                                                                  147 AAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAAT
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1 (bases 1 to 1052)
Zhang J. and Williams, N.
Purification, cloning, and expression of two closely related
Trypanosoma brucei nucleic acid binding proteins
Mol. Blochem. Parasitol. 87 (2), 145-158 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/organism="Trypanosoma brucei"
/mol type="mRNA"
/strain="TREUG67"
/db_xref="taxon:5691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="RNA binding protein"
/protein_id="AAB81433.1"
/db_xref="GI:2554935"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 t
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76. .915
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Matches 76; Conservative
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SOURCE
ORGANISM
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ACCESSION
VERSION
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                            /translation="MANTYDELYVPLSYYILQNEGGNTSKIDQANTKKPKKEVINKS
SLIIDIKPYGENTDLDEVLKLVKNITMEGLTWGKAHKKTPPAFGLFKLQVSCVIVDDL
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Join (10556 . 10737,11044 . .11146,11373 . .20416,20578 . .20690)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="gynonym: PFC0875w"
join(10596. 10737,11044. .11146,11373. .20416,20578. .20690)
/gene="MAL3P7.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /notes Revised: added 3' exon, possibly spliced at 5' end, revised: added 2x 5' exons by similarity with P. knowlesi; signal anchor predicted by Signalb 2.0 HWM (Signal peptide probabilty 0.001, signal anchor probability 0.997) with cleavage site probability 0.000 between residues 36 and 37 Pfam match to entry PP00005 ABC_tran, ABC transporter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPYFILLFFYNI IFTLVVYFYVYKCLMNYFILPFLIYPFLMNSLLFTI CMOPSNNSS
YNYAFTLFFPLRSSFRLI HGGASTLTFPVLLTPHSSFCLLSLDF IFLIKNNI KID
YNYAFTLFFLENS SFMLI LIGS I WSTATTFPVLLIPHSSFCLSLDF IFLIKNNI KID
YNGLFIKFRNI SLMHLI I GSI YNYEVLLI CILNY I YYKKKAMMLNYFYKRGKSKS I TN
DKRKKSQQKTYEFGNINY DMSEKY PTHQLKDNSNDFMLEGSDEDDTCYFLDTLHKKOY
NOGMULRI EKK KNDRRESHRYDI PHP LARHNNI INNNI NINNI NINNI NINNI NINNI NINNI NINNI NINNI NINNI NINNI NINNI NINNI NINNI NINNI NINNI NINNI NINNI NINNI NINNI NINNI SKDSGNSTLL I QURKKKDI KROVANI TRKOM
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YENLTFYETIKIFLLYYNKNVDKYLNKKRTLKIMNDLDLVQYLNDQIKNLMDEVKKKI
SIFICFLVKRDIYILDEPFIALDIKTKTKLFKFPDKIKKNNIIFICTHDIYEANNFAN
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MYNNHNKYGKYKONNNNNS PYNARDDTELTD I EBNI SSKKKKNKFI EKEFSYNTYRNN
KNNDENDEYGBYDNYDDNMI MSNTSNI MKKKNI KKONI PKTCINPFTTY I KPTLLLKL
                    1.1e-15, 53.2% identity in 141 aa overlap, revised:
bortened exon 2, aplicing confirmed in P. knowlesi; Pfam:
match to PP00736 EF1BD, EP-1 guanine nucleotide exchange
domain Score 61.10, E-value 7.9e-22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILVTNINEFTNNRDI IKKNI IKFI KGTRNENKNCPI PPNENHI YCTYKINELESLKKL
LCVLNKFKNI LTYQLKTI DI YYTY I YI YTLNEKKKLLKNI QDKDI KYLI BI DPLFPLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIAVIKSGQIIPKGSKNSFQKLIEYKPTLNIQPNGLPNEEQTNYLSQEKIMSALNKKG
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                                                                                                                                         /codon_start=1
/product="elongation factor 1 (EF-1); putative"
/protein_id="CAB39068.2"
/db_xref="G1:8052274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3; Length 253305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="transporter, putative"
/protein_id="CAB39024.3"
/db_xref="G1:23477031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.1%; Score 48.4; DE
57.1%; Pred. No. 1.6;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              score 72.50, E-value 9e-18"
                                                                                                                                                                                                                                                                                                                           /db_xref="GOA:097319"
/db_xref="SPTREMBL:097319"
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Best Local Similarity 57.1.
Best Local 88; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /noce="Similarity: to kinesin-related protein.
D.melanogaster kinesin-like protein 67A (TR:P91945) BLAST
Score: 664, sum P(2) = 1.9e-67; 28# identity in 707 as
overlap; Pfam: match to PP00225 kinesin (6.1e-86), Kinesin
motor domain Score 311.54 E-value 6.1e-86
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NRLTEGDIVIVFSQYGEFIDVNLVRDNETGKSKGYCFLSYADQRSTILAVDNFNGYKL
LERPLVVDHILNYRLPKKYLKDADKNEYKPTGAEGQGIGVYNVVESEIKLSKVFDKIK
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DDBDDDDDSVDI KYKRHKEKRKSLTTKKYDKKEKHKRKSDHRDKHRRRENHSRHREK
EKDKKSHKRRHKHSYDKYSSRSRSYSTSSSTDR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Similarity eg to C.elegans RNA-binding protein (TR:01818) BLAST Socre: 379, sum P(1) = 3.8e-35; 37% identity in 297 as overlap; splicing conserved in P. knowlesi and P. yoelii; Pfam: match to PF00076 rrm, recognition motif: (a.k.a. RRM, RBD, or RNP domain) Score (58.01, E-value 1.1e-20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIHLTSIDTISKIHARDLLKENKRKLENPQENIKHEHKDEVSLYVKKKKIKKKAM"
join(5457. 5577,5689. 5787,5923. 6077,6189. 6743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(5457. .5577,5689. .5787,5923. .6077,6189. .6743)
gene="MAL3P7.2"
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/gene="WAL3P7.3"
/note="Similarity to P. falciparum elongation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="RNA-binding protein, putative"
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/bx.rxef="GA:097318"
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organism="Plasmodium falciparum 3D7"
mol type="genomic DNA"
isoTate="3D7"
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|gene="MAL3P7.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_gtart=1
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                                                                                                                         db_xref="taxon:36329"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GOA:097277"
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                                                                                                                                                                                                                                                                                                                                                                                                        gene="MAL3P7.1"
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                                                                                                                                                                                                                                                  gene
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contig of 100 bp

: gap of 100 bp

: gap of 100 bp

: contig of 1037 bp in length

1: gap of 100 bp

2: contig of 931 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                gap of 100 bp
contig of 986 bp in length
gap of 100 bp
gap of 100 bp
contig of 953 bp in length
gap of 100 bp
contig of 1010 bp in length
gap of 100 bp
contig of 1033 bp in length
gap of 100 bp
contig of 1033 bp in length
                               35: contig of 927 bp in length 35: gap of 100 bp 4: contig of 927 bp in length 4: contig of 979 br
                                                                                                                                                                                                               v: gap of 100 bp
1: contig of 961 bp in length
1: gap of 100 bp
1: contig of 885 bp in length
2: gap of 100 bp
: 100 bp
y of 957 bp in length
f 100 bp
g of 968 bp in length
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g of 929 bp in length
f 100 bp
g of 921 bp in length
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of 1018 bp in length
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contig of 969 bp in length
gap of 100 br
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of 1008 bp in length
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of 912 bp in length
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contig of 944 bp in length
gap of 100 bp
contig of 947 bp in length
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contig of 942 bp in length
gap of 100 hr
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of 991 bp in length
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contig of 997 bp in length
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of 973 bp in length
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contig of 964 bp in length
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of 901 bp in length
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gap of 100 bp
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of 875 bp in length
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of 903 bp in length
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Birran, M., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Gamarater, J., Campopianor, A., Chang., J., Chospel, Y., Colangelo, M., Collins, S., Collymore, A., Chospel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Pitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gradam, L., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Line, W., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., McCarthy, M., MacGonald, P., Marquis, N., Mathews, C., McCarthy, M., MacGonald, P., Marquis, N., Mathews, C., McCarthy, M., MacGonald, P., Marquis, N., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., McDeeters, R., Meldrim, J., Meneus, L., Minovan, C., McCarthy, M., Phukhan, P., McKernan, K., McDeeters, R., Meldrim, J., Meneus, L., McEwan, P., McCandald, P., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Retta, R., Riley, R., Rise, C., Rogov, P., Roman, J., Retta, R., Riley, R., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Stange-Thomann, M., Schupback, R., Stojanovic, N., Strauer, S., Schupback, R., Ye, W., Travers, M.
                                                                                                 Homo sapiens chromosome 11 clone RP5-873F21 map 11, LOW-PASS ACCOLLS SAMPLING.
                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I to a9989)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo gapiens chromosome 11, clone RPS-873F21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This record contains 38 individual
* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: 1.12134
Center clone name: 873_F_21
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1038: gap of 100 bp
2183: contig of 1145 bp in length
                       35400 AAAAAAAAAATGGAAAAATGAAAATTAAATTA 35367
   146 AAAGCAACGCTTGAAAAAGGAAAGTTAGCCCTA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                         AC091136.2 GI:17047133
HTG; HTGS PHASE0.
HOmo sapiens (human)
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                                                                                             RESULT 22
AC091136/c
LOCUS
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KEYWORDS
SOURCE
ORGANISM
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Barna, N. Bastien, V. Baloen, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Charag, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., PitzGerald, M., Cage, D., Galagan, J., Gardyn, S., Gord, S., Graham, L., Grand-letre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., McCarthy, M., Meldrim, J., Meneus, L., Mhova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., Phunkhang, P., Plerre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Wo, A., Wilsen, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (06-MG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Aug 6, 2002 this sequence version replaced gi:12740251.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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93546: gap of 100 bp
146150: contig of 52604 bp in length.
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    146150
    organism="Homo sapiens'
/mol_type="genomic DNA"

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Homo sapiens chromosome 11 clone RP11-222M17 map 11, WORKING DRAFT SECUENCE, 5 ordered pieces.
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Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-222M17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 GAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 ATACTACRTGTTCTCTTCTAAGTCCCACTCCTCTGTTTTCTTTGAGCAGGAAAGAGAAAG
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                                                                                                                                                                                                                                                                                              DB 2; Length 39989;
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9.1%; Score 48.2; DB 2; Length 399
Best Local Similarity 52.3%; Pred. No. 1.9;
Matches 127; Conservative 1; Mismatches 114; Indels
                                                                                                                                                                                                                3932 others
                                                                                                                          /map="11"
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8024 c 7083 g 10567 t 3932 ocl
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HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
HOmo sapiens
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AC021298/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50037 AAAACAGAGCTTCATTTTACAATGACAGACCCCTTTATCCTGAGATAGGAAAGGGGGGAAA 49978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50217 ATCACTATACCTGATTATGAATGATTTTATTTCCTTTGTTATATGATTCTCTATTCCAAA 50158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50097 AACGTCACTACATTGAGTATTATGACACAAAATTCTTGTATTTAGATTGCTACTCTCCAC 50038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC124657 155985 bp DNA linear PRI 18-AUG-2002
Homo sapiens chromosome 11, clone RP11-624D11, complete sequence.
AC124657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 ATTTATATGGTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTATTCCCAA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches 114; Indels
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Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-624D11
                                                                                                                                               ieature 51443. .55402
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ieature 55503. .9346
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ieature 93547. .146150
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45160 a 28301 c 28298 g 43985 t
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                                                                                                49624. .51342
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49624. .51342
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                                                    clone_end:SP6
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Stojanovic,N., Strauss,N., Subramann,A., Talamas,J., Tesfaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
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Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (18-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 18, 2002 this sequence version replaced gi:22123120. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Only the last 156.0 kilobases of this clone are being submitted.
The remainder overlaps accession number AL358944 (Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 624_D_11
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complement (15331. .15556)

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complement (15708. .15842)

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5240. 15264
                                                                                                      /rpt family="(T)n"
                                                                                                                                                                                                                   rpt_family="MIR3"
157. .4648
                                                                                                                                                                                        rpt_family="L2"
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57319 ATCACTATACCTGATTATGAATGATTTTATTTCCTTTGTTATATGATTCTCTATTCCAAA 57260
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Homo sapiens chromosome 11 clone RP11-802012 map 11, WORKING DRAFT
SEQUENCE, 16 unordered pieces.
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Birran, B., Linton, L., Nuabaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguelawkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 11, clone RP11-802012
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Pred. No. 1.8;
1; Mismatches 114; Indels
                                                                                                               /rpt_family="LTR16C"
complement (22698 . 22946)
/rpt_family="LIM4"
22947 . 23343
/rpt_family="MLTIJ1"
24245 . 24502
/rpt_family="MLTIJ1"
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25311. .25454
/rpt_femily="L13"
complement(25491. .25513)
/rpt_femily="MERSA"
25514. .25533
                                                                                                                                                                                                                                                                                                                                                                                            /rpt family="(CAAA)n"
complement (25534. .25598)
/rpt family="MER5A"
complement (25599. .26466)
                   /rpt_family="MIR"
complement(22125. .22227)
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.21799)
                                                             /rpt_family="L1M4"
22264. .22287
/rpt_family="AT_rich"
complement(22347. .22
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HTG; HTGS PHASE1; HTGS DRAFT:
HOMO BADIENB (human)
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Best Local Similarity 52.3
Matches 127; Conservative
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9746 ATCACTATACCTGATTATGAATGATTTTATTTCCTTTGTTATATGATTCTCTATTCCAAA 9805
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936 98366: contig of 13391 bp in length 3867 98466: gap of 100 bp 467 117242: contig of 18776 bp in length 1343 147820: contig of 18776 bp in length 1821 147920: gap of 100 bp 6821 147920: gap of 100 bp 1821 181996: contig of 34076 bp in length 1920 1000 pp 1000
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147921. 181996
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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakorque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Melous, L., Mihova, T., Miranda, C., Mengay, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, M., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Wyman, D., Ye, W.J., Pieter, Submission
                                                                                                                                                                                                                                                                                                                                                                                              Submitted (108-MAY-2000) Whitehead Institute/MIT Center for Genome Submitted (108-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 9, 2000 this sequence version replaced gi:7717156.

All repeats were identified using RepeatMasker.

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
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Insert size: 180496; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; agarose-fp
Quality coverage: 4.6 in Q20 bases; sum-of-contigs
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Consensus quality: 117141 bases at least Q40
Consensus quality: 176943 bases at least Q30
Consensus quality: 179052 bases at least Q30
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of 13941 bp in length
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of 5822 bp in length
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of 7644 bp in length
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of 4661 bp in length
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of 5134 bp in length
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Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 bp
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PTNSFRKSTYGSVSSPSSSNKDSIKLGDEPAIREALKEFRSDENDIDWVLFGYEGGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NI INNOHINHOPNHYINNINNINNINNINNIND BDINNI HFSINIGIMMI I YNPILLSNFNINNINNIN MINNINNINNINNIN GENI YALLSKL
MYNINNINNINNINNINNINNINNINNINNIN GENI YN YAMDAROHEGELIKTDEROOKKHRES BINBFITLISKL
ATKSDLOSI DLI PEREKSKYMDLINIPLHYI EERGELLIKTDEROOKKHRESDKINBEKREK
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CDS predictions from GeneID do not necessarily reflect true genes. Further Information is available from IMB Jena, Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(9422. .9434,9523. .9686)
/note="GeneID exon scores (in order of location ranges):
1.55, 2.07 - GSCJ_ID dd_00861"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (join(10316. .11073,11163. .11973))
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/note="GeneID exon scores (in order of location ranges):
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Slime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="similar to Dictyostelium discoideum
mold). Homeobox-containing protein (Fragment)"
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/db_xref="GI:28829237"
                                                                                   and the Univerity Colonge, Institute for Blochemistry (http://www.uni-koeln.de/dictyostellum/project.shtml Punding
                                                                                                                                                                Deutsche Forschungsgemeinschaft (DFG)
Location/Qualifiers

    .36188
forganism="Dictyostelium discoideum"
/mol_type="genomic DNA"
ferrain="AX4"

                                                                    (http://genome.imb-jena.de/dictyostelium/)
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                                                                                                                                                                                                                                                                                                            'db_xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSNGNNFSPESAMSVSKLISD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YIIYNVKYRLIAYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
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                                                 Genome Analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250083 CATTATGCAATAACATATTTACTTTTATTAAAATAGTATCATAGGAAAAAAGGGAA 250142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250143 AACGTCACTACATTGAGTATTATGACACAAAATTCTTGTATTTAGATTGCTACTCTCCAC 250202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A linear INV 12-MAR-2003 map 6061442-6097630 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 ATTTTTCTTAAGCAAATATTT-CTTTGCTAATCAATAAATTATCAAAAGAAAAAAAACT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 GAAAGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 ATACTACRTGTTCTCTTAAGTCCCACTCCTCTGTTTTCTTTGAGCAGGAAAGAGAAAG 264
                                                                                                                                                                                                                                                                                                                                                           82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence and analysis of chromosome 2 of Dictyostelium discoideum
Nature 418 (6893), 79-85 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.

1 (bases 1 to 36188)
Gloeckner, G., Elchinger, L., Szafranski, K., Pachebat, J., Dear, P.,
Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K.
Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 4 (bases 1 to 36188)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 36188)
                                                                                                                                                                                                                                                                                                                                                           26 ATTIATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTCCCAA
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                            1
                                                                                                                                                                                                                                                                  Length 256221;
                                                                                                                                                                                             2101 others
                                                                                                                                                                                                                                                             Score 48.2; DB 2; Length 2
Pred. No. 1.8;
1; Mismatches 114; Indels
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fragment chain:1
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vector alde:right"
a 51050 c 48305 g 76442 t
                           fragment:01174
                                                                                                fragment:06229
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Dictyostelium discoideum
    137037. .248507
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                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.3%;
Matches 127; Conservative
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AUTHORS
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AC115608
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248507: contig of 111471 bp in length 248607: gap of 100 bp 256221: contig of 7614 bp in length.
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119039: gap of 100 bp
129647: contig of 10608 bp in length
129747: gap of 100 bp
135936: contig of 7189 bp in length
137036: gap of 100 bp
                                                                22137 bp in length
                                                                                                                                                                                                          100 bp
of 3786 bp in length
100 bp
                100 bp
of 2097 bp in length
100 bp
                                                                                             contig of 5280 bp in length
gap of 100 bp
                                                                                                                              contig of 2466 bp in length
gap of 100 bp
                                                                                                                                                                7058 bp in length
                                                                                                                                                                                               5506 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment:00955.0"
6466. 38014
force="assembly_fragment:01016"
88115. 41034
note="assembly_fragment:01599.0"
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119040. .129647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="assembly_fragment:00208"
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                                                                                                                                                                               100 bp
                                                                                 100 bp
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/chromosome="11"
                                                                                                                                                                contig of
gap of 100
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                                     contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP1-13519"
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1. .2923
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97158:
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65234
67245
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69542
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                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                            AL356371 256221 bp DNA linear HTG 20-OCT-2001 Homo sapiens chromosome 11 clone RP1-13519, *** SEQUENCING IN PROGRESS ***, 22 unordered pieces.
9926 AAAACAGAGCTTCATTTTACAATGACAGACCCCTTTATCCTGAGAAAGGGGGGAAA 9985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M7815; 1$ '1$ 'of reads
Sequencing vector: plasmid; L08752; 98$ 'of reads
Chemistry: Dye-terminator ET-amersham; 2$ 'of reads
Chemistry: Dye-terminator ET-amersham; 2$ 'of reads
Consensus quality: 250899 bases at least Q40
Consensus quality: 252999 bases at least Q20
Consensus quality: 252999 bases at least Q20
Insert size: 254121; sum-of-contigs
Insert size: 354121; sum-of-contigs
Unsert size: 38381; 1.2$ error; agarose-fp
Quality coverage: 9.35x in Q20 bases; sum-of-contigs Quality
coverage: 25.82x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                            Craniata, Vertebrata; Buteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                          Submitted (16-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jun 28, 2001 this sequence version replaced gi:14529810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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of 11980 bp in length
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of 11549 bp in length
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of 11417 bp in length
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gap of 100 bp
contig of 3307 bp in length
gap of 100 bp
contig of 7855 bp in length
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of 2920 bp in length
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100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 bp
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Web Bite: http://www.Banger.ac.uk
                                                                                                                                                                                                          AL356371.18 GI:14575185
HTG; HTGS PHASE1; HTGS_CANCELLED.
Homo sapiens (human)
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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gap of 1
contig
gap of 1
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Direct Submission
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52652
                                265 CAG 267
                                                                                                                                               AL356371
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                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                             DEFINITION
                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                               RESULT 26
                                                                                                                              AL356371
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.13824)
                                                                                                                11.45, 37.54 - GSCJ_ID dd_02158"

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TESNOTLLTWESEFGADVKKDLINFESKSVGLNLQDLQKFFSK"
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NSISRPGGLEVLEVEIHSDTDQLKLDHLKSTVSKVPSLIINNCQSKEIIIDTLKHMNQ
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                                                                                                                                                                                                                                                                                                                                                                            PEYSYNONICINSEEERHRYGYOXCKENOQAFCNV"
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PWSLDGGRIAAYFLGYTSHQAAPDFGYDCGGLANESEAAHWPPFLRAATKYLLETYPO
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TNFTTI YGQNMY SYRGKDI RSKDLNGGFDDLI I SSPGFGVPGSMQTCCYYY I I SNGS
SYTLOGGSGFTSED DQVATCKLGNETHARKGWNI PULDLBYLDRIDGI FULI I IGAPSSS
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NLLLSI KGFTKXSR RGGSLL GKLLESTDEFARLBYGARPLUTDS I DNLSGFVEIKN
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NLLLSI KGFTKXSR RGGSLL GKLLESTDEFARLBYGARPLUTDI DNLSGFVEIKN
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COMPLEMENT (join (5915. .6290,6400. .6732,6912. .6940,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cränslation="MGFLTLIKKFWAMVEKGKVFVTFSVLSVWFGESVISIKTFQYDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="similar to Homo sapiens (Human).
Phosphatidylinositol-glycan-specific phospholipase D 2
procursor (EC 3.1.4.50) (PI-G PLD) (Glycoprotein
phospholipase D) (Glycosyl- phosphatidylinositol specific
phospholipase D)"
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2.23, 56.16, 218.21 - GSCJ_ID dd_02155"
                          Direct Submission
Submitted (12-MR-2003) Genome Analysis, Institute of Molecular
Submitted (12-MR-2003) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
On or before Mar 4, 2003 this sequence version replaced
gil:20081115, gil:20081115, gil:20081117, gil:956926.
CDS predictions from GeneID do not necessarily reflect true gene
Further Information is available from IMB Jena, Department of
                                                                                                                                                                                                                                                                                   (http://genome.imb-jena.de/dictyostelium/)
and the Univerity Colonge, Institute for Biochemistry
(http://www.uni-koeln.de/dictyostelium/project.shtml
Funding
                                                                                                                                                                                                                                                                                                                                                                                                             Agency: Deutsche Forschungsgemeinschaft (DFG) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Dictyostelium discoideum"
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                                                                                                                                                                                                                                                           Genome Analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
   AUTHORS
                                                              JOURNAL
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                                                                                                                             COMMENT
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CDS

SOS

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/translation="MIPNYDILIEFLSSVTNIIPPLELKISNIKEPLSGKLGTILLMQ
join(22161. .23091,23307. .23707)
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GRGRAYSVSSSSSASTGGGRANTGKTFRAAGSKFTPSAVPKSGGSTLGFPDBQQVRDT
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FWNHLIYBVSRYNHFYSTIINGDNLANSKIDIFKELIPGIYNTINRSHEBVLANEENFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="MDEDNNDRIEFLFWKVFRNKYIFNEIFYIIKNTEWVQYIDPSEI NIDNKCSIFETYSFELMIKNKLFEVLIEKRYDDK NIDNKCSIFEKRYGFEVQKKVBNQFLETKRYBDDK ALBIEKRNGFECOLTELAIEYENVE ALRILINGPYNLFYRESSFELAIEYENVE ALRILINGPYNLFYRESSFELAFKKTRNLTIVKELLNGTRALINDNYGFDFITKREFK
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HNCTRFLUSSFVIKKLIDLAVICNFBNEKHALISKIKADCSMETLGSLSSIYTRFYS
CEKESEINTKYLQEQLELIYAKKKALLEFPIKDLKINFSKIFFNQPQSMYNCEVIR
DTTTNBIIDFKYYVDDIYMDEQRNELYFNSILKCDIETLKKIDSLDLASVDKTICLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKNGLPNMTNEDGMKVLNYLNDNGFKSFEVSGELCLFLRHFLINIIIPPNFKLNLQLP
SQTDINHRFLIYVFSLSFKSLRLFINSMDSISTITKLNITRHNYTEKSDEIFDIYQOIQ
YYCHDNGFIDIDNFIEIIELFLKKFHKNNNNNNNNNNNNNNNNNGFESLEEDADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDYVITRILNFFFLILIKTKGVKIDOVRYVHNLLSEVSITIDHGICHVFFYLNIRSPK
FSKYIINLPGIKVFIDIFNRGVLNGSEFSGNNSTHTVFGVNLFKCFNLNDFSFDYVIG
ENENHEKVGSFLDILNKLIESFSINLYNHAFSNNSKTSLKSDYFHDQPNYDLQFLLEI
RRVDSFFKYLQWIQLNCQHYQNIRNEQFTYNSPFHLKKPTKNDQIGSSSPPPFSHSTI
                                                                                                                                                                                                                                                                                                                                                                                                                           DNSEEEEQEEEIDDKNGNNNNDNEEDENAHNHNNDNNEDIEFNDDDDNNNEDIEFYD
GDDDNSDDBMEIDDSRRLPLEMFFIQPNIQQILKSLVDQHLNSLISKRKNHLFKSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MCDKIEILFWKVFKNQYLFNEIFNQIHNNQWIEYDDPNKYNVYN
RGKFGDTHSLLIMLENDLLPLIKDKIKHGDHIEITYDSMLELFSKLSTEPSINSNKNK
NKYKDEDYLKIIELLMKHRRDEFEVFDLIMMAVSSRSPDVIRLLVNEPYSVIIYPTML
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QSDTQLYFKSALDQILLRIEEKSYEINSPFNENLENPFLESFIYGDIKTCNIILKYYP
NQFKITKDSITKTLEKEKINIIKYYYKVENCKNLINNFKNDNNLLKHLKNELLNHPMY
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FFVSFFQNEI YSFSLFYSREDLILFILINNYNI DI DLHPPLFKPDRGHSQYLECKPI FE
NHPEKVKNI SKLNLKQKWFELRCLQPPLVLLNSFFKY I CKEKNI TRYNQFI QNDNLQI
     NTIILLGKGNGGVNELISNLQDNLVGYGLVRIVEKIDNSDTIKFAYINWIGEEIPRMI
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                                                                                                                                                              complement (12821. .13888)
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17246. .21229
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LYKKNLNVIELLLKSFDNFNFIHQPEQMSAIVDKERNLFHISGELFQVDKKFSFQIIR IIKLIMDKFNKLTKDQINIENISTTTYRLFLNYLYDQLLRVKGLTIDQLEYVRSIIPE QLANNNFETYRIFFYLNIRSSKLSNYLJKRPGITYFIRNSTELLYNNFYNTAEPITDE IGFPLLKKLARFELFTYDILGKELANOYNNSGCSGCSSGSSSSSSSSSGGDDGKNN KKYITOPDILLKELIKKLSKNIKCHRSDBLYVELPSPSTTTTIRFFLKIDNFER PIPNKSTIKVNWNSDKLIQLFKPISKLINSFKYSDGVMESICRVMTVNEIORFIOYN Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 5441)
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2 (bases join(23880. .23905,24093. .24438) /note="GeneID exon scores (in order of location ranges): -3.80, 10.29 - GSCJ_ID dd_03433" Sequence and analysis of chromosome 2 of Dictyostelium discoideum Nature 418 (6893), 79-85 (2002) Submitted (21-MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 54441) Direct Submission Submitted (04-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 4 (bases 1 to 54441) 144 TGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAA TGATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTATATTTCCC CESFFONEIYTYSVFFSRDDLMSFLLNNFNIDIDLHFPSFEPNRGYSQYLE" Dictyostellum discoideum chromosome 2 map complement (3622543-3568102) strain AX4, complete sequence. AC115584 AC117266 AC117268 AC117270
AC115584.2 GI:28828280 Score 47.8; DB 3; Length 36188; Pred. No. 2.4; 87; Indels The Dictyostelium Genome Sequencing Consortium Pred. No. 2.4; 0; Mismatches REFERENCE

INV 12-MAR-2003

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Location/Qualifiers
1. .162554
/organism="Homo sapiens"
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6261. .6476
/rpt_family="MIR"
7016. .7295
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4608. .5023
/rpt_family="MaLR"
                                                                                                                                                                          MAPPING INFORMATION:
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                                                                                                                                                                                                                                                                                                         106738 ATTTACATCTGTAATTATGAGTGATTTTTCTTTCCTCTTTAGATTTTTGGAATTTCTCA 106797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Jan 9, 2002 this sequence version replaced gi:14550326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRI 09-JAN-2002
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Submitted (28-AUG-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 162554)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                86 ATTTTTCT----TAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAAA 141
                                                                                                                                                                                                                                                                       26 ATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTATTCCCAA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butherla, Primates, Catarrhini, Hominidae, Homo.
1 (Bases 1 to 12254)
Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION SEQUENCE BAC Clone RP11-1145F21 from 2, complete sequence. AC079354
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Center code: WUGSC
                                                                                                                                                                                            Length 152336;
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Armstrong, J., Cotton, M., Hawkins, M. and Dignan, G.
The sequence of Homo sapiens BAC clone RP11-1145F21
Upubblished (2001)
3 (bases 1 to 162554)
Waterston, R.H.
                                                                                                                                      855 others
                                                                                                                                                                                                                                 47; Indels
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                                                                                                                                                                                          Score 47.8; DB; Pred. No. 2.2; 0; Mismatches
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86817._.119636
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                         clone end:T7
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Best Local Similarity 63.88
Matches 90, Conservative
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                                                                                                                                    51773
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                    BASE COUNT
ORIGIN
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TITLE
JOURNAL
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AUTHORS
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TITLE
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AUTHORS
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REFERENCE
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LOCUS
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all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (1.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
this sequence was finished as follows unless otherwise noted:
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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

名 ઠે 셤 ò

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 5:1:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bappac.med.buffalo.edu)

NECTOR: pBAACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-107N15, 2000 bp overlap; the clone sequenced to the right is RP11-68606. Actual start of this clone is at base position 1 of RP11-1145P21; actual end is at this clone is at base position 1 of RI base position 162554 of RP11-1145F21.

Data from AC069148 and AC064836 was used to finish this clone,

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------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                  Chemistry: Dye-terminator Big Dye; 94% of reads
Chemistry: Dye-terminator Big Dye; 94% of reads
Assembly program: Phrap; version 0.966731
Consensus quality: 135985 bases at least Q30
Consensus quality: 135985 bases at least Q30
Consensus quality: 144829 bases at least Q30
Insert size: 145000; agarose-fp
Insert size: 145000; agarose-fp
Quality coverage: 3.9 in Q20 bases; agarose-fp
Quality coverage: 3.7 in Q20 bases.
* NOTE: This is a "working draft' sequence. It currently
consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
      2000 this sequence version replaced gi:5932616.
On Apr 13, 2000 this sequence version replaced gi:593: All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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gap of 100 bp
contig of 18346 bp in length
gap of 100 bp
contig of 18295 bp in length
gap of 100 bp
contig of 28139 bp in length
gap of 100 bp
gap of 100 bp
contig of 28139 bp in length
gap of 100 bp
                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                    Center clone name: 363 G 1
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
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contig of 5484 bp in length
gap of 100 bp
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3739. _9222
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      COMMENT
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SDQLIRYISSINKKITKYFHVESIMDDGSYAHDDTPTIQSILVDNPQITDLKHTKFVF
TVQKQLFNDLYNGNEPFNTNVLNDLLSFKENVIFLYKK"
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                                                                                                                                                                                                                                                                                                                                                                                                                           'translation="MQIFIKTLTGKTITLEVEGSDNIENVKAKIQDKEGIPPDQQRL1
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'codon_start=1
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Pred. No. 2.3;
0; Mismatches 42; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C. and Lander, B. Homo sapiens chromosome 4, clone RP11-363G1 Unpublished
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Best Local Similarity 63.5%;
Matches 73; Conservative
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ion 2903729333 /note="AluJb repeat: matches 1299 of consensus" ton 2988830195 /note="AluY repeat: matches 1308 of consensus" ton 3028930601 /note="AluSx repeat: matches 1311 of consensus" ton 3077830937		3130731608 /note="AluSq r	n ~ w	/note="L2 repeat: matches 26062691 of 3219932315	/note="MER5B repeat: matches 60177 of 3240132488	/note="L2 repeat: matches 2452. ,2550 of consensus" 32903. ,33206	/note="LiM2 repeat: matches -517. ,-221 of 33241, ,34061	/note="L1M3e repeat: matches -455368 of 3473935429							3813938833 // // // // // // // // // // // // /	3884139840 /note="1.10%13 renear: marches 4195 518	3984339876	70000 1 000000 2 000000 1 000000 1 000000 1 000000 1 000000	40873. 41084 renear marches 5769 5974 of of	4106541373	/note="Alusc repeat: matches 1297 of cone 4137441623	/note="Lim44 repeat: matches 59/4 6300 of 4163441856	/note="L1M4c repeat: matches 18111627 of consensus 4194342051	/note="AluSg repeat: matches 1109 of cons 4206842344	/note="LIPA4 repeat: matches 58616142 of consensus" ion 4234542553	/note='		-	4 /	4 /	4376744004	. 4 >	48015. 48129 48015. 48129 xmonst. matches 30 142 of CC	4813448314
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right end of clone RP11-317C20 is at 56073 in this sequence. Location/Qualifiers 1182012. / organism="Homo sapiens" / mol_type="genomic DNA" / ch_xref="taxon:9606"		W _ C	(1	/note="L2 repeat: matches 25662749 of con 31103345	/note="MIR repeat: matches 21. 39274102	/note="88 copies 2 mer tt 57% conserved" 41084406	/note="AluSx repeat 62776330				/note= 18 copies 2 mer tc 94% conserved"			n 1099811075 /note="3 copies 26 mer 92% conserved"	1111111148 /note="19 copies 2 mer ac	1150712390	15656. 11873 vancet. matched 5201orso or 15656. 12673 vancet.	/MOCESTIFICS TEPERC: MACCINES 35%/olfs 1638716491 //orbotal.FF1.ma resear. matched 32 127 06	165571641	17439 17610	/note="MIR repeat: matches 49241 of conse 1958420420	/note="LIPAS repeat: matches 53086143 Of 2081321163	<pre>/note="THELA repeat: matches 1354 of consent 2116422730</pre>		n 2273523078 /note="THE1A repeat: matches 3354 of consensus"	2371924027	25619	2578425850	/note="MER5B repeat: matches 103173 o 2613026262	/note="MER5A repeat: matches 7141 of consensus" n 2688427199				
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This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known amnotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Ems. BMBL; Sw., SWISSPROT; Tr., TREMBL, Wp., WORWPEP; Information on the WORMPEP database can be found at http://www.ananger.ac.uk/Projects/C_elegans/wormpep This sequence throw as generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL359846 182012 bp DNA linear PRI 16-DEC-2000
Human DNA sequence from clone RP11-413C10 on chromosome
9q31.1-31.3, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (16-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: Humquery@sanger.ac.uk Clone
requests: clonerquest@sanger.ac.uk
On Dec 9, 2000 this sequence version replaced gi:11557924.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                          Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
http://www.sanger.ac.uk/HGP/Chr9
http://www.chori.org/bacpac/home.htm
http://www.chori.org/bacpac/home.htm
http://www.chori.org/bacpac/home.htm
This sequence is the entire insert of clone RPII-413C10 The true
left end of clone RPII-31J20 is at 123231 in this sequence. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 182012)

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AL359846.11 GI:11611367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSD QNEIGSTIEELOGOOTVOTISTPAPKKHNTTTTTASPSYSSOPAPOPPOOSOO
IDGLDDLDELMESLNTSISTALKAVPTTPERHTTHANSNSPPSLHKNTSSTNSASSL
SERNNNDSVSYSTPOPCKYTSTATITTKKQPALSKATLETTSCHNVYSSOPSOSOPOY
KVTRATNSQPSSDDLDELLKGLSPSTTTTTVPPPVQRDQHGHHHQHHHHHHNNNNNN
TQTVTTQINICRTNTPNNNNNNNTNSPKVVHGDDLDNLLNNLTSQVKDIDSTGPTSRG
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AVECAHCDEPISBCTTALGKKHVHHPEHFVCQPCLKSPEGGNFPERBGGRPYCBADFYSTP
AVRCGGCNSPIRGECINALGTOWHPEHFVCQYCQKSPTNGQPFEFGGRPYCDVHYHOO
AGSVCSGCGKAVSGRCVDALDKKWHPEHFVCAPCMNPLAGGSYTANNGKPYCKGCHNK
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EFLCFSPLEFRAGSTVOTVWRQIGAQLQNFYSESLSENDLINBEBSENRKRKIGGNBNS
GSLASGGNNTPVKQKKKKQDQKQDVKEKEKEKEKEKEKEKEKEKTRTTTTTTTAN
ANSNBLSNSGGGNSSKKLNESSDSTQSDSTNRTKPNANPNTTSIRKKKKKGGRGGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'translation="MESPNVEILFWKVFHNKYLFSIILKBIHKCEWVNYVYLGYHVDN
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protein id="AAM44367.1"
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                                                                                                                                                                   protein"
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db_xref="GI:21240657"
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                                                                                                                                                              product="hypothetical
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PTSGOITINGHDLVTDRAQALRGVSVCPQFDALITLFAREQLSLYCAIKGVPDDKIS
LVVEAFIKMADLGKIANSVTGGSYGGNRKRVSLSIAMLGNSSVLIDBEASGCDPIIR
YRQCOVISELGKNKVIILTSHSMSEIQALGSBWTIREDGGPKCLGGSTQHIKSKFGAGY
SVEVKFKKSCLEVGIPQSLQCVLECFPNATILDQHDLMASLELPNPPENPIKVSEIPN
ILSTELSSILDDYSVSQTSLEQVFLKTTGATHEDRLAINNQQQQQTIPNSD"
COMPLEMENT (join (7575 . 8146, 8235 . 8364))
// note="ORF ID ad 02702"
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FNWILKLIRKNNSSEVEVGLIALQSLLLKDDFRIFFNNIDGSALLLINILQALSTSSVN
IQLLYETIYAIWLLTYNKDIAAAYSGTGLVANLVQLVKTVAKEKIVRLSLSTLRNLLN
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ISGELEWTPVHKSERFWKENISKFEENNYQVIKHLHQILKTSQSTPLQLSIACHDLCE
FVRHHSRGKAIMTITNQTRYHGYDVKSNEEVKNQALFALQKMMLNNWEYLNAK"
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Ynliskydkhtdaekkekpaansasyvnffvnpinstsnieiiqylltlineiieidp
                                                                                                                                                                                                                                                                                                                                                                              SISEVDVY FKEINDKSEMENY FQINSTQVFGGIWFESNQLSSVANTTNTNTTTNSFKY
SIRLDSNSVLDSNKVKDNGIDSSDYLTKNWAY IQIAMDQAI FGY FGLDYKLVINGQRY
PDPYVELWQKWINGRESVFKSAGSVFVSAALLI FTFRLVTELVVEKETKIREGMSIMG
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VLVQLFKPNYDLIKTTQFSNRINENNIIIYGGKAGSLNVEQKGVIDMMKFQLSNELNK
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protein id="AAM44363.1"
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CDS

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AC123513 61052 bp DNA linear HTG 29-MAY-2002 Dictyostelium discoideum chromosome 2 map 2779865-2840915 strain AX4, *** SEQUENCING IN PROGRESS ***.
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                                                                                                                                                                                                                                                                                                                                                  61 TCTTTATACTTTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAAT 120
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1 (bases 1 to 61052)
Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P.,
Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K.,
Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                                                                                                                            /codon_gtart=1
complement(join(1193. .1583,1653. .6117,6198. .6330))
                                                                                                                                                                                                                                                                                                         Gaps
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NOTE: This is a 'working draft' sequence.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
Location/Qualifiers
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                                                                                                                                                                                                                                                               DB 3; Length 6457;
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                                                                                                                                                                                                                                                                                                       39; Indels
Deutsche Forschungsgemeinschaft (DFG)
Location/Qualifiers
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    . 6457
    /organism="Dictyostelium discoideum"

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/strain="AX4"
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join(448. .628,705. .803,875.
/mote="ORF_ID:dd_02708"
                                                                                                                                                                                                                                                             Score 47.6; DB
Pred. No. 2.8;
0; Mismatches
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                                                                                                                                                                                                2765
                                                                                     /mol_type="genomic DNA"
/strain="AX4"
                                                                                                                               /db_xref="taxon:44689"
/chromosome="2"
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                                                                                                                                                                     /map="209116-215573"
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HTG; HTGS PHASE2.
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Dictyostelium discoideum
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Best Local Similarity 64.5%;
Matches 71; Conservative
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REFERENCE
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KEYWORDS
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                        FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                86 ATTTTCT----TAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAA 141
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Gloeckner.G. Eichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K.,
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
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of
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Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular
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                                                                                                                                                                                                                                                                                                                                                26 ATTTATATGCTGATTTATGCGTGATTTTGCTTCCTTCTTTATACTTTTATTTTATTCCCAA
                                                                                                  4; Gaps
  'note="AluJo repeat: matches 120. .287 of consensus"
                                                                /note="L1ME repeat: matches 704. .839 of consensus"
49993. .50299
                                            .503 of consensus"
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and the Univerity Colonge, Institute for Biochemistry
(http://www.uni-koeln.de/dictyostelium/project.shtml
Funding
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Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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                      49601. .49693
/note="LIME repeat: matches 421.
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                                                            .49947
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Matches 90; Conserv
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complement (join(124605. .24844,24917. .25293,25414. .25489))
/note="GeneID exon scores (in order of location ranges):
22.64, 31.07, 2.50 - GSCU_ID dd_01626"
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/db_xref="G1:2882382"
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NKFDKINGDSSICFSOVGGFRVLEFSSGLGNSEIFTVKSEEDYYFEEYDHYBTCKHQ
IGITDLHVKPNQKLRNKTFYFFVQEBYYYSGCRNIYLKNCDIKTDQKNDSISYEIQIL
KIHSPLNISHSTIPSFHIFFTIFFILFFLIFFTSNSLFSSLINISGGWGLISDFGKR
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GMAAFKEISPANGTKLKNSLNGATVFLIIATFVVLGIPKASREDCEDYAKDSSLNYTG
SQVDEMCGGDIYKKFIGSHTDEDGSKLSWGPTTAWIAIVVGLGIAFFNNIFVYCGPVF
RS"
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TPTPAPILTSTLSVNSTSSSSKLQBKALPTKTTFITQTSSPLLLPQPLTSTSTSTST
TSTSTSTSTSTTTIPTPTTSSFKSNSFSTSNDNSNNNNNNNNNNNNNNNNNNNN
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                 OFKQLTDQTTHLADQAAIYQQNNKELKLELEKSQDELTIERKRVIKLQDETLRTPQV
XIPSPSLGSNIPGGANNNNNNNNNNSNNNNINNNGNNMGGSGSSSLASSTNGINKQQS
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DSFNLIFYLLIYIYHPCKSNILVKRLNSYYDDGDELSINQNQSQQKSIDEINLY
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/note="GeneID exon scores (in order of location ranges):
249.99, 106.06 - GSCJ_ID dd_03289"
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phosphoprotein (Dentin phosphophoryn) (DPP); Dentin
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/protein_id="AAO51012.1"
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/translation="MRSTSKNGSFNLIKNIFIYNVGEYILTSDSFPKKVSEIDFIFVF
/translation="MRSTSKNGSFNLIKNIFIYNVGEYILTSDSFPKKVSEIDFIFVF
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    (bases 1 to 163443)
    Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B. and Davis, R.W. Direct Submission

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L. Submitted (05-37N-1999) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA.

**OTE: This is a "working draft" sequence. It currently consists of 1 contigs. Gaps between the contigs.

** NOTE: This is a "working draft" sequence. It currently are represented as Tuns of N. The order of the pieces are represented as Tuns of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

** This sequence will be replaced

** by the finished sequence as soon as it is available and

** the accession number will be preserved.

** This sequence will be replaced

** by the finished sequence as soon as it is available and

** the accession number will be preserved.
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/note="GeneID exon scores (in order of location ranges):
24.05 - GSCJ ID dd_01625"
/codon_start=1
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Hyman,R.W., Pung,E.L., Qin,F., Rowley,D., Mao,J., Tamaki,T., Kurdi,O.B., Conway,A.B. and Davis,R.W.
Plasmodium falciparum 3D7 chromosome 12
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Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum

    163443
/organism="Plasmodium falciparum"

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57.3%; Pred. No. 2.5;
+ive 0; Mismatches
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/db_xref="taxon:5833"
/chromosome="12"
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Best Local Similarity 57.37
Best Local 86; Conservative
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AC117070 AZ15976
                                                                                          EQRTPLILTQKSLTSKSLANIAVTSTSDSDGIKPKFIYSEFFEBDDEDEGSDEESDED
DEDEESDEBYREEDGFNDLEDDEEDQNNSYVQDLTKQIEKHFSLNDEKKANNNNNNSQ
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Dictyostelium discoideum
Lubasaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 136240)
Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K.,
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Sequence and analysis of chromosome 2 of Dictyostelium discoideum
Nature 418 (6893), 79-85 (2002)
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Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular Submitted (12-MAR-2003) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany On or before Mar 4, 2003 this sequence version replaced gi:20042931, gi:20066187.

CDS predictions from GenelD do not necessarily reflect true genument of the contractions of the contraction of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                      24 TGATTTATATGCTGATTTATGCGTGATTTTGCTTCCTTCTTTATACTTTTATTTTCCC
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and the Univerity Colonge, Institute for Biochemistry I
(http://www.uni-koeln.de/dictyostelium/project.shtml
Punding
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Location/Qualifiers
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Pred. No. 2.6;
0; Mismatches
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oin(12993. .13277,13378. .13450,13554. .13748,14017. .14609,
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CNKLEI NNNGSI NVENNSKI NLNGGL I MKDKSQI YLNNSNI EI NGDAMLANQSI FNTM
NNLDLFI SGSLHLNDDSLFLLFDNNEMTI NGDLLLNGI SKLFVNDKSELSI YGDLKI N
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STIFNSDIVVVIIDSVFKSHSLIVNKSSLAIGNSIIVSDDLIINESEETHFTYVY
IEGGNSILQNSSYIRLADSIFIINKGNLIIHPNSYINLENSKFILDNGIVKTSGRLYI
NNNSTFEINQNGIYNLSSGGIYYTNDTNIKSNNITLKNDGIFNIDNDNVEINISFINN
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LINRVDFENAMDNLLPKDNITESFEFLSSYITEPVTLDEKYTLDQSLQKKVQKTQSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tränslation="MKKIFLPIIFLIILIIKLSNCDRLVYVGDRNNKQSFLNKTNWYP
EKVPTKDDSLLLSNGGNLLIDYDEICSSEYFTINNGSFYLYGQYSVYDSMDINRGSFI
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/note="GeneID exon scores (in order of location ranges):
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14702. .16798)
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/note="GeneID exon scores (in order of location ranges):
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (eIF3); Suilp {Saccharomyces cerevisiae}"
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/db_xref="G1:28828359"
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db_xref="GI:28828358"
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QHLAAKELKKKSWKYHKKYTTWLPDFNTIKILNEQVEHGTYVSFDYVSTWSKQLKKN
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ve 1; Mismatches 95;
                          401. 8444
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8487. 8510
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12406. 12439
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.1237. .11271
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12695. .12736
                      rpt_type=tandem
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Matches 104; Conservative
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BYDYQKLDNYK INKRANFTFF I NI TYMEP FRYYDEKKKT SYTD I PRYMYKKKYVSS
I YKKKQCKNT I WILL I ARKGSLHEKKTKE I LGDPVYNYBEKGE I SYTD I PRYMYKYKKYSS
I YKKKQCKNT I WILL I ARKGSLHEKKTKE I LGDPVYNYPWE I SI PFHET I TREQS PY YN
PLKGEWAYLDYKRDSRRACGKI EGGLENYDGKGLKLEKGVDR PRYKEI PYYLDHGVEW
SKDLSNIL I YPNHKAENH I PYGYRGPSGFT PEPKLEWELARGE FRAYEYDPVL
SKDLSNIL I YPNHKAENH I PYGYRGPSGFT PEPKLEWELARGFFRAY FDDPNWM
I KYYRI TKKL I LEWHEADKNSTKI DKI KSELFGI TSRKKYTSNOI KL I NEHALLRAKE
I LLDHILLOPRONDPDYI TYYLDHGHEP IDYI GGGNHKCSBEER I KKRYTVLANKCYFEDPWM
SLLAHILOPRONDPOYTYTYDHGHEP IN TSREKKYTSNOI KL I NEHALLRAKE
HETYSSINSI PERABWHYTYWTEI RGEGRI NILSEDDVEDKFQCYFELQHDRKNFPALU
SLYKPLMSNNYYLE
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KNEWTNNPLADNKNERIHKKREAILEEVIPAKI JDTYRNNRNQDMNKNVKNESVRSCI
SCPCGWDADDEAMNEILLEEREKKLKLLEEEREKTKLLLEEEERERERIKLLEEEEKER
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3472. .3503
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Plasmodium falciparum 3D7

Plasmodium falciparum 3D7

Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 250029)

S Gardner, M. J. Hall, N. Fung, E., White, O., Berriman, M., Hyman, R. W., Carlton, J. M., Pain, A., Relson, K. E., Bowman, S., Paulsen, I. T., James, K., Bisen, J. A., Rutherford, K., Salazberg, S.L., Craig, A., Kyes, S., Chan, M.-S., Nene, V., Shallom, S.J., Suh, B., Peterson, J., Angiuoli, S., Petrea, M., Allen, J., Selengut, J., Haft, D., Mather, M.W., Vaidya, A.B., Martin, D.M.A., Fairlamb, A.H., Fraunholz, M.J., Roos, D.S., Ralph, S.A., McFadden, G.I., Cummings, L. M., Subramanian, G.M., Mungall, C., Veneer, J.C., Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Fraser, C.M. and Barrell, B.
  INV 07-0CT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 419 (6906), 498-511 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (13-SEP-2002) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
Location/Qualifiers
1. .250029
                                                                 146 AAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAA
                                                                                                                                                                                                                                                                                               AE014830 250029 bp DNA linear INV 07-OC
Plasmodium falciparum 3D7 chromosome 10 section 2 of 7 of the
                                                                                                                                                                                         206 TACTACRIGITICICITICIAAGICCCACTCCTCTGTTTTCTTT 247
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/isolate="3D7"
/db_xref="taxon:36329"
/chromosome="10"
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/locus tag="PF10 0059"
join(<1560. .2109,2341.
/locus_tag="PF10_0059"</pre>
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/rpt_type=tandem
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/rpt_type=tandem
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1240. .1274
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289. .1319
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/rpt_type=tandem
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/rpt_type=tandem
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697._.757
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AE014830 AE014185
AE014830.1 GI:23494922
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*** SEQUENCING IN PROGRESS
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    (bases 1 to 196149)
    Hyman,R.W., Fung,E.L., Qin,F., Tamaki,T., Kurdi,O.B., Conway,A.B. and Davis,R.W.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases I to 196149)
Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
Direct Submission
Submitted (21-May-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto,
94304, USA
On Apr 2, 1999 this sequence version replaced oi:4117171
                                                                                                                            26 ATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTCCCAA
                                                                                                                                                                                                            AAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAA
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    Gaps
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* NOTE: This is a "working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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HTG: HTGS. PHASEL.
Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum
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47831: gap of unknown length
179129: contig of 131298 bp in length
179329: gap of unknown length
196149: contig of 16820 bp in length.
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Mismatches 109; Indels
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/db_xref="taxon:5833"
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  Matches 113; Conservative
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FRQTACGTGTPTHKQCRCDDKAAVDPPTYFDYPQYLAWFEBWAEDFCRKKNKKLKDV
KTNCRDGSTGPTHKQCRCDDKAAVDPPTYFDYPQYLAWFEBWAEDFCRKKWKKKLKDV
KTNCRDGSTGPTYGSGAGGASCGASCRAFRAATIKYEGYBKKFYBERKKRHTDNQKLE
GLLANBKACKDINEEKRIDFTKAVEDDKNINKEGTFYHSQYCQPCPGCGMKKTKNGN
GWEEKDTWGONIKLYKPTSSAKFTEIKLKSGERHDDIKERIBQKCKTONGSDGSGG
NSEKKELYDBKKCYQTGELTKOOGGGWDDPPYDRLUSTGGCCLGLENOKKKESDPKS
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/db_xref="G1:234945275.1"
/tb_xref="G1:234946275.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLKYGKTAPTGWKCVTPSGDKAATSSEGKGSSDGGAKDGVGVNGGALQRNKRDLATPS
AKSGDTTGGKDGATGKSDGSICVPPRRRRLYIQKLHDWAEKVGDTATQPQVDTPSQSD
KLRDAFIESAAVETFFLWHRYKKIKDKEKLEEQQRQRENGELPGLSSSGDGDSNDPQS
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SISYYENSGYTPTPPWYENYTPQYWELHGHHWGANICALFYKENGIDKPBYDTA
VRAQLWDSGKNTPQNSKYQYTNYKLEEEZGAKINI PDTSGDNTPTLAYPTLKRFVEI
PTFFRWLHEWGSDFCRQRKRMLKNYKHNCRNI ERGGHEYCGGDGHDCTRDGI QHNNML
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RSFDQFLISLKHCKNNEGDGSDPKNKIDFKEPLKTFGPLEYCKTCPPNKVNCNGPSRR
SGGNDQCTAVNGNEWEKIFSENGGNSTIDVHMIDRRGPYMEKKSQKLENSENPLFKT
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LKKRKIEBKCTQKGEKTCDDESKNDCACVKKWVEKKTTEWEQIKEHFKNRNQKDGDGN
DMKSSVRQLLDPLIYRMDLANGKGKINELKEFLKSYECKCVDNAGNSEKDVVECLLQK
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MLONOPKDVPNDYSSGDIPPNTLYFDNNOEKPFITSIHDRNLYTGEEYSYNVNM
VNNDNIPINRDNNPYSGIDLINDSLNSNKVDIYDELLKRKENELFGTEHHPKHTNIYN
                                                                                                                                                                                                                                                                                                                                                                                         NKKI EGNKNNCGACAPYRRLHLCHHNLES I DTTSTTSDTLLAEVCYAAKFEGETLTTQ
HGQHQQTNPGTASQLCTVLARSFAD I GD I VRGKDLFLGNDEEKKKRDELEENLQK I FA
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KEKGINKILDBEKKREEBERADGYVGYNSGGANQNNTTIDKLDHEDRDATKGNGO
EPTKPASKPEDLARGSGASPDTPREDSPPADLDDEEHDBDDEDBDDAEEBEBEEKKEE
BEEHKEEENBAAPEEKKEGGSSPEEVEEKAKBAPAGPDACNIVQTLFSSIDKFSDAC
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PSPPI PPLATSTLAWSVGI GFAAFTY FYLKKKTKASVGNLFQI LQI PKSDYDI PTLKS
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17pt type=tandem

13562. 13586

17pt type=tandem

16563. 16614

17pt type=tandem

17p15. 17943

17pt type=tandem

17p15. 17943
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/rpt_type=tandem
12960. .13070
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12966. .13039
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13048. .13072
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9334. .19422
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20141. .20273
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20940..21079
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                                                                                                                     86 ATTITICTIAAGCAAATATTTCTITGCTAATCAATAAATTATCAAAAGAAAAAAAAACTG 145
                                                                                                                                                                           AAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAA 205
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Length 252650;
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 2148 03-JAN-2002;
                                                                                                                                                                                                                                                                linear
 Score 47.6; DB 3; Length 2 Pred. No. 2.4; 0; Mismatches 109; Indels
                                                                                                                                                                                                                                      206 TACTACRIGITCTCTTCTAAGTCCCACTCCTCTGTTTTCTTT 247
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/mol_type="genomic DNA"
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Sequence 2148 from Patent WO0200928.
AX347077
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PFWALIP2_2 200001
PFWALIP2_3 300001
CONTINUATION (2 of 4) of PFWALIP2
   9.04;
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Best Local Similarity 52.8
Matches 102, Conservative
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Best Local Similarity 50.9
Matches 113; Conservative
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PFMAL1P2
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ORGANISM
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PFMAL1P2 1
WPCOMMENT
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AX347077/c
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AUTHORS
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VERSION
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CYGSCEKKLIQTIEGFIGGFGSFVPDNLDMKPLFCCPEKKKNSTISRLHLMDIYTNKT
ETTIPYRIVKEINLINBLNDPPIYISLNTLQGVIYIVYTVKCSYVYVFDEGTLSLIVKE
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VLSYINNFKQINFDYVGIFITIVNYEFPQGNADNKDSAFVGDFNSGSKNETMDFFNDG
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KRAGARVILSRGSIEJWKVALDETUKYKRNYTDQY1GSTLIESNNADEITYVYKAFIE
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AAVAYEYKLREEAFVIYKKENCYTSAISVLLDKILYNKNQKNKNFHEFSSHDSTVPYY
SNNNNKONITEGKKSDNENDEYLKQFYONSYREKYGSYYNNDISNSNNNIHHAPER
NNEDKFSSDTLLHNYED IDSTESTCDLSNYEDDLANAIESTEAGKCNNNDWFILGSRAQLK
LINKIIDSIDSFVKSNNPRAYKEVIEKCKENNPYEHLITYLNTREQNSLKDVLVDSEL
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VYDPYIEBENLANYNLIKILENKINDNRIVQTKIKKSNNLAPLIQKYEDIQAQNITAV
NSTLABIYLQNDDVISLANSIDEYDNFNQYRLLANKLENHKLEBENRIALALLYKKOKKY
KEAINLSKKEKQYKDAIEIARVSKONVYIEDLINYFIESKNKEAFCACLIVCYDLLKP
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NNQFNYSLNNNLSIMPPQNNFMSSNSFDKYDMFNNNTHF"
3056. .3105
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LKLKEYALAIEAAKKAKSLKTWKEVNFICVKYKQLKYAHTAGLQLIMHADHLDEIIKI
YEKKKYINELMNLLENGLNNERAHVGIYTELGILYAKYKPEKLMEFIRNYTNKMYTRK
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/translation="MSQNNPLSVCVADNLINYDIQNESFRLGNVSVEGDKYICVKENV
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KI CSLALAEYMYWKWI NNDTIAI VCEKNVYHWNI DIHNTKKNKONNDNNNNNNNNNNN
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/note="HMMPfam hit to PF00637, 7-fold repeat in Clathrin
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/locus tag="PFL0935c"
complement(join(<11613..12941,13715..>19156))
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protein id="AAN36274.1"
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<2608. .>8601
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<2608. .>8601
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/rpt_type=tandem
1758..1801
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2150. .2184
/rpt_type=tandem
2301. .2344
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8716. .8742
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1484. .2513
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9080. .9130
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                                                                                                                                                                                                                                                                                                                                                                                    101168 ATAATACTTTGTTAAAATATGTAACGATTTATAAATATGTGAATATATGCAATATAAA 101227
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1. (Dases 1 to 252650)

2. (Dases 1 to 252650)

3. (Darder, M.), Hall, N., Fung, E., White, O., Berriman, M., Hyman, R.W., Carlton, J.M., Pain, A., Nelson, K.E., Bowman, S., Paulsen, T.T., James, K., Eisen, J.A., Rutherford, K., Salzberg, S.L., Craig, A., Kyes, S., Chan, M.S., Nene, V., Shallon, S.J., Suh, B., Peterson, J., Angiuoli, S., Petrea, M., Allen, J., Selengut, J., Haft, D., Mather, M.W., Vaidya, A.B., Martin, D.M., Fairlamb, A.H., Fraunholz, M., Subramanian, G.M., Mungall, C., Venter, J.C., Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-SEP-2002) Stanford Genome Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA 1 (bases I to 25250)
Hyman, R.W., Fung, E., Conway, A., Kurdi, O., Mao, J., Miranda, M., Nakao, B., Rowley, D., Tamaki, T., Wang, F. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE014847 252650 bp DNA linear INV 11-FEB-2003 Plasmodium falciparum 3D7 chromosome 12, section 4 of 9 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 419 (6906), 498-511 (2002)
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Submitted (29-JAN-2003) Stanford Genome Technology Center, Stanford
University, 855 California Avenue, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                      203
                                                                                                                                                           84 AAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAAAC 143
    24 IGATITATATGCTGATITATGGGTGATITITGCTTCCTTCTTTATACTTTTATTATTCCC 83
                                                                                                                                                                                                                                                                                                                  144 TGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAA
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Nakao,B., Rowley,D., Tamaki,T., Wang,F. and Davis,R.W.
Direct Submission
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/organism="Plasmodium falciparum 3D7"
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/isolate="alpan": Ab
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/rpt_type=tandem
96. .134
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/rpt_type=tandem
1220. .1250
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1331. .1363
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AE014847 AE014188
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9.0%; Score 47.4; DB 9; Length 176109;
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1926. 1940.

1936. 1940.

19564. 20147

1000-"similar to EST AA034047 (NID:g1505856) zi05e04.81"

20436. 20733
                                                                                                               MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequence of this clone between the NHGRI Chromosome 7 Mapping Project (Exic D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/CTB/CHR7, send mailto:egreen@nhgri.nih.gov or see http://genome.wustl.edu/gsc
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                     Clone CTA-250D13 is from a release of the human BAC library CITB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from VECTOR: pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEIGHBORING SEQUENCE INFORMATION:
The actual start of this clone is at base position 1 of RG250D13;
actual end is at 176109 of RG250D13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST W21257 (NID:g1298308) zb58b07.rl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="CTA-250D13"
/clone_lib="CITB-HS-A"
5770. _5950
//note="miniar to EST T97069 (NID:g735693) ye50f03.rl"
5770. _5949
/note="miniar to EST AW490098 (NID:g7060333)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone contains STS 8WSS2794 (NID:g1113588) and 8WSS350 (NID:g484309).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .176109
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/mol_type="genomic DNA"
/db xref="taxon:9606"
/chromosome="7"
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15790. 16074
16787. 16890
/rpt_family="L2"
16787. 16890
/rpt_family="MIR"
17143. 17416
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/rpt_family="MIR"
18853. .18989
/rpt_family="Alu"
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/rpt_family="MIR"
15633. .15723
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/note="similar to
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15108, .15194
/rot family="L2"
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4806. .15107
rpt family="Alu"
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EST AW946860 (NID:98124633)" /rpt family="Alu" 37807 37949 /rpt family="Alu" 38095 38581 /rpt family="MalR" 38876 39185 /rpt_family=Alu 39402. .39485 /rpt_family="L2" 39826. .39926 /rpt_family="MIR" 41270. .41572 /rpt_family="CR1" 44716. .44926 /rpt_family="CR1" 47256. .47583 /rpt_family="L2" 26006. .26319 /rpt_family="Alu" 6377. .26788 /rpt_family="L2" 28294. .28390 31078. .31146
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69975 TATATGCGTACTGAAGTATGCCTATTTATACTATTTATGTTTACAAATATATTTTTTATAT 70034
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AC003992/c
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                                                                                                                                                                                                                                                                                                                                                                                                     156060 bp DNA linear HTG 12-AUG-2C Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN AC004153
                                                                                                                                                          CITCCTTCTTTATACTTTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
2 (bases 1 to 156060)
Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
Direct Submission
Submitted (18-FEB-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto, 94304, USA
                /note="chemically treated genomic DNA (Homo sapiens)"
1174 c 22520 g 54649 t
                                                                                                                           Gaps
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HTG; HTGS PHASE1.
Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 156060)
Hyman, R.W., Fung, B.L., Qin, F., Rowley, D., Mao, J., Tamaki, T., Planai, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
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* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                        Length 113515;
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                                                                                                                      77; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:5833"
                                                                                        DB 6;
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/db xref="taxon:32630"
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/clone="3D7"
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          outmitted (14-JAN-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, 4 (bases 1 to 176109)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (03-FRB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, 5 (bases 1 to 176109)
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Missouri 63108,
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Homo sapiens BAC clone CTA-250D13 from 7q31, complete sequence.
AC003992
                                                                                                             159 AAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minx, P., Hinds, K., Sutterer, C., Becker, M. and Ozersky, P. The sequence of Homo sapiens BAC clone CTA-250D13 Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Genetics,
Park Avenue, St. Louis,
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Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Submitted (14-JAN-1998)
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University, 4444 Forest
6 (bases 1 to 176109)
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Direct Submission
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate

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Submitted (13-SEP-2002) Stanford Genome Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA (13-SEP-2007)

Hyman, R.W. to 250707)

Hyman, R.W., Fung, E., Conway, A., Kurdi, O., Mao, J., Miranda, M., Nakao, B., Rowley, D., Tamaki, T., Wang, F. and Davis, R.W.

Direct Submission

Submitted (29-JAM-2003) Stanford Genome Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA (1-250707)

/organism="Plasmodium falciparum 3D7"

/mol type="genomic DNA"

/isolate="3D7"
                               Lebraryotta; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Lebraryotta; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

Gardner, M.J., Hall, N., Fung, E., White, O., Berriman, M., Hyman, R.W.,
Carlton, J.M., Pain, A., Rutherford, K., Salzberg, S.L., Craig, A.,
James, K., Eisen, J.A., Rutherford, K., Salzberg, S.L., Craig, A.,
Rypes, S., Chan, M.S., Nene, V., Shallom, S.J., Suh, B., Petcerson, J.,
Angiuoli, S., Pertee, M., Allen, J., Selengur, J., Haft, D.,
Mather, M.W., Vadoya, A.B., Martin, D.M., Fairfamb, A.H.,
Fraunholz, M.J., Roos, D.S., Ralph, S.A., McFadden, G.I.,
Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C.,
Barrell, B.
                                                                                             22654 AAAAAACAAAATTTCACAGAAATCATAACATTTTTCAAAAATAAAACATAAAATGTAAG 22595
                                                                                                                                    AE014848 250707 bp DNA linear INV 11-FEB-2003
Plasmodium falciparum 3D7 chromosome 12, section 5 of 9 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 419 (6906), 498-511 (2002)
                                                                   2 (bases 1 to 250707)

Hyman,R.W., Fung,E., Conway,A., Kurdi,O., Mao,J., Miranda,M. Nakao,B., Rowley,D., Tamaki,T., Wang,F. and Davis,R.W. Direct Submission
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75.-406
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477.-541
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rpt_type=tandem
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AE014848 AE014188
AE014848.1 GI:23496770
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/rpt family="MER1_type"

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14707. 14756

/rpt family="Alu"

17097. 17812

/rpt family="MeR1_type"

/rpt family="Alu"

/rpt family="Alu"
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12Dt family="MIR"

20224. 20267

12Dt family="MER1_type"

12028. 20570

12Dt_family="Alu"
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2057]. .20700
/rpt_fam.ly="MER1_type"
 /rpt_family="L2"
9202".9391
/rpt_family="MER1_type"
9392..9678
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14124. .14359
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/rpc_family="MER99"
19429. .19573
/rpc_family="MER1_type"
19579. .19647
/rpc_family="MER99"
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1972. .14123
pt_family="MER1_type"
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/rpt family="MalR"
31219. 31329
/rpt family="MalR"
31422. 31509
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7. Tept family="ERVL"

7. Tept family="L2"

10573...10593

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7. Tept family="MIR"

10594...10917

7. Tept family="MIR"

7. Tept family="MIR"

7. Tept family="MIR"

10902...10937

7. Tept family="MIR"

10918...11169
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2196. .32302
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29065. .29261
/rpt_family="L2"
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29262. .29555
/rpt_family="Alu"
29556. .29941
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                                                       3392. .9678
/rpt_family="L2"
9679. .102^*
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family="L2"
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_family="L2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 176379)
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Park Avenue, St. Louis, Missouri 63108, USA
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                              51 TTTGCTTCCTTCTTTATACTTTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTT
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Homo sapiens BAC clone RP11-504020 from 2, complete sequence.
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The sequence of Homo sapiens BAC clone RP11-504020
Unpublished (2001)
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Contact: sapiens@watson.wustl.edu
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Genome Res. 8 (11), 1097-1108 (1998)
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  Pred. No. 2.7;
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                      0; Mismatches
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University, 4444 Forest Pi
6 (bases 1 to 176379)
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Matches 63; Conservative
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The clone sequenced to the left is RP11-514D19; the clone sequenced to the right is RP11-53A12. Actual start of this clone is at base position 1 of RP11-504O20; actual end is at base position 176379 of
                                                                                  all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong vBCTOR: pBACG3.6
clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                           Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. 1 MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                The RPCI-11 human BAC library was made from the blood of one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613. 716
/rpt_family="L1"
/rpt_family="MBR2_type"
1215. .2157
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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8470_.8545
/rpt_family="MER2_type"
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/clone lib="RPCI-11"
513. .716
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5224. .5561
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/rpt_family="L1"
2158. .2449
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/rot_family="L1"
/2904. 3100
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/rpt_family="L1"
/674. .809^
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4686. .4879
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2450. .2728
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8186. .8256
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1937. .4069
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                                                                         Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA, UK
On or before May 14, 2001 this sequence version replaced gi:2982540, gi:2982541, gi:2982554, gi:2982556, gi:2982556, gi:2982556, gi:2982556, gi:2982556, gi:2982556, gi:2982556, gi:2982556, gi:2982556, gi:2982556, gi:2982556, gi:2894491, gi:2982556, gi:2894491, gi:2892556, gi:2894496, gi:2894380, gi:2894588, gi:2894589, gi:2982539, gi:2894380, gi:4725992.
For more information about this sequence or the Malaria Project, see http://www.aanger.ac.uk/Projects/P_falciparum.
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D.melanogaster kinesin-like protein 67A (TR:P91945) BLAST
Score: 664, sum P(2) = 1.9e-67; 28# identity in 707 as
overlap; Pfan match to PP00225 kinesin (6.1e-86), Kinesin
motor domain Score 311.54 E-value 6.1e-86".
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DIHLTSIDTISKIHARDLIKENKRKLENFORNIKHEHKDEVSLYVKKKKIKKOM"
join (5457. 5577)5689. 5787,5923. 6077,6189. 6743)
/gene="MAL397.2"
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/note="Similarity eg to C.elegans RNA-binding protein

/rr.0181818] BLAST Score: 378, sum P(1) = 3.86-35; 37$

identity in 297 as overlap; splicing conserved in P.

knowlesi and P. yoelii; Pfam: match to PP00076 rrm, RNA

recognition motif. (a.k.a. RRM, RBD, or RNP domain) Score

/codon_start=1
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PFWAL3P7

PFWAL3P7

PISSENGUIUM falciparum MAL3P7, complete sequence.

NA AL034559 AL008975 AL008981 AL008981 AL0091015 AL010169

AL010187 AL010189 AL010157 AL010167 AL010160 AL010165 AL010169

AL0139179 AL84502 298556 298557 298558

AL034559 4 GI:8052273

AL034559 4 GI:8052273

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AL034559 6 AL01188 AL0118 AL0118 AL01188 AL021888

AL034559 6 AL01188 AL0118 AL0118 AL0118 AL01188 AL01188

Nacetylglucosamine-1-phosphate transferase; protein, kinase; R-FA3 repeat; regli; repli; repeat; repeat; regli; regli; RNA-binding protein; plasmodium falciparum 3D7

ENARYOTS T-Complex protein 1 epsilon subunit; telomere; var. plasmodium falciparum 3D7

ENARYOTS Alveolata; Apicomplexa; Haemosporida; Plasmodium.

ENARYOTS Alveolata; Apicomplexa; Haemosporida; Plasmodium.

S. Lawson, D., Basham, D., Brown, D., Chillingworth, T., Gentles, S., Gwilliam, R., Harris, D., Holroyd, S., Hornoky, P., Jagels, K., Jassal, B., Kyes, S., McLean, J., Rajandream, M.-A., Rutter, S., Skelton, J., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Squares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S., Stares, S
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                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCT 218
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SYSKWEKHENENKCHKLI I KYE I KNYPDI I UN LINKCKENYLNNNLYDDI I YN I I YNTRDN
YLSLKSLLLI SNS FI KLYP TRET FYNYI FI HI LKLCKENYTINNLYDDI I YN I I YNTRDN
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INDWSREGYLKGYGYEFR LOONDY INTROCHI KNSOKI LLKI I SKWKKK I TA
NDDMSREGYLKGYGYFR FRODNIN L'INKOCHI KNSOKI LLKI I SKWKKK I TA
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SPETENNNKI TILNDTHLHILLMILIKKGFINGDVIKYISNETMYHEYYKGUKNAS
LYLFFHYHRNSLINGPENNN FCTLMHROMITYHCHOYPFSSTLLIGSNQLKYGKGYYN
ILDTSILNHLKEIYFNKHVDISLNDMKNIVDFVFYFNKSITGNYLKAEYRKIKNSNDK
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EKKNK I NKVN I KNVY PHNNKNI YNDANMYNHNQHDI SI DTSYKNHHTHQCVKI NNY I S
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YNMMSIYTPFIAPKKCCNKKKPVYFFSNNSFCKIYLMKFSFNIRMFILIKQIVEYLLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGYNKKYVGSVAYRLYKIVKMNVYTMKGGYVYLHKPKQKIPKKK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .>3709
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                              .1655
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                           repeat_region
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CDS

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FINSEHYKKENINKYQLOHKNI KOVI KESINLELLELLIKUSLDEQKETQQPWICKETYSDVE
KELYEKRENENIKKQLIKHI YNNGNNTKQSKYI QINNTGSCNEHNI LIMKKKKKKKKKKTTYSDVM
ETKNSHLI KELI EKKKKLI SKYLONNNNNTKKHI FKYI KTKDY INCHNGNHLI INFEN
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YLKYFLEONYFVLLI HGFDTHGL PIEYNWKLLIKIK HI QDLALNSSY THRONBELKOH
HVFPKSY INLLINKLKNOHKKKROS FELNEN FERNI I SKOTI EQOKI STFKNICKSJA
SYPVNBQPMSLVSY GI WGYNNYTY ITPYKPYEQI ONKYFRDLLKYY YTHSNRE I YHS
YATKTYLSDSEI I YKKNVNYTY ITPYKPYEQI ONKYFRDLLKYY YTHSNE PIYHS
KAYNSFEDNILTKYY KKYKLUJITOWHT FRUNKCLI HEKYLY RI HILKY BDEKENOFFI I CD
KAYNSFEDNILTKY YSKKSPI KEI KNI CTFQCNS FMSCTY KNFTNNEENNFI FYSDNEI
KSSYRGT VHYAPSHGFTDYNFY YTRONKLKKTY YLDI SRY GEI EKENOP
NDWIKARSYSKI FNENNSLSLDY INENNWHOBUDLKDEYTEL VYKNLEKNIHFI
KKSFTRENSLSKYTHEN SKYNSLSLDY INENNWHOBUDLKDEYTEL VYKNLEKNIHFI
KKYKTTERSNAQSILNSLDI MKKKTKKLAIN INENDIHSLFFYSFYENILL YYFPYENILLY
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                                                                                                                                           KYEKLIWERVLENNI EKRMI KRKI ENMDAKI KLANSFRHI NKYNKYVANKFCKKWKKR
KYELIKCHTAISQY I DTNNI J DLLYYTLITTITY YYMNI CSQONNI KINSSFI ITYEKP
I I PI LINKAYLLKKEQI VININY YLYKONLCI HTLKYVHYKLYKSYY I LAYWKEI I LIK
I LQRNKTFKNYMDFI HFNNNSRTSNNA I QNI EKNE I HKENSTYMYLLANY PSI SQTSYK
                                                                                                                                                                                                                                                                                                  YKLQNDVNKNILGNNLHYKNTQFYKNIVHHNLYQQFSYLQNASHQLYMYFIYFQKKLK
GRNMSLIFNGKYIKKEIKRRKKGRINRMNIINTIKLNKTSFLYNDANHKETKRKKNTS
                                                                                                                                                                                                                                                                                                                                                                 ILLKONIELLTVKKTYILHNHLJQVHYKAKSKSTNIMMATNENNIYVEPIYSSNNINQ
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SRQKYWGVNIPLKDIELDQNQKIIFNNQIMDVWFDSSVSYIYVLYMCKHILFHTYFNK
EKYY FKININQFI I LIMVKLLSINVY EI VKKI INSLININY TYLY I NINKS YVKKNKI I INNY FL
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PIKAVI VHNYVVDSANI KMSKSLANVI SPRELFFEKEKDDI PTTSKRKDTQKPDDLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKHFNIFLCCEGIDQIRGWFQSFFFVFFCLNWINQRKKTRSQLLKNTDKIIDKKGVVI
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gene mRNA

CDS

Gaps Length 250707; ö 87; Indels DB 3; Score 47.4; DE Pred. No. 2.7; 1; Mismatches 9.0%; 99; Conservative Query Match Best Local Similarity Matches 99; Conserv

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/ LFARS 1 at ion = "WKI RKLYGLLKKI YYEKRKDFFLY FFLLI PFLLI SFHLFLRNI
SDRYSLEI YNTSPED SPRÜKTINDTIRQYVLFLSBELGSKEINDE YVHILCTPCHELM
KDFLSYAENNDLMI FRLYNSEEDCLKALKTATIELKSEDFKNYNSLELNDDI LINIHEND
KNOELLYNLATHYI INIKASSERVINDL XXOVY PENEFBAI KNIKLINPHI LIKVVKHYBERYK
NFIKDI KNILKNENHYTOY FNDDRKKLFFYNFVKNNLVFTKY SCGLLSVENVNYYKKOK
NYKESYLFGLSPOSSERGKGLYKOLKANPLYNKENKOY GONPFHLY YPYTLEBEDDKAINE
KNERNEKNERNEKNERNEKNGENEKNOLI LESTNNNVNKROKIG GSYHNNNS INSN
DOQKKKNNNNNNYYYYNNPDGLITNVKYKIRVGDYALLANSNEKY FFNDININLKONPI
NENTYDDLSFNI YENEWYYFSFFI VLEYQFNSFILLNSNAEKY FFNDININLKONPI
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INFRATODLSFNI YENEWYYFSFFI VLEYQFNSFILLNSNAEKY FFNDININLKYYYYYYSML
INFRATOTRERNAENNESNEKNIN I STRUKYYYYYYSWL
INFRATOTRERNAENNESNEKNIN I FTLLVVY FYLLINGNAENT I CMQFSNNSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Join (10596. 10737,11044. 11146,11373. 20416,20578. 20690) join (10596. 10737,11044. 11146,11373. 20416,20578. 20690) /gene="Malabry.4"

/note="Revised: added 3' exon, possibly spliced at 5' end, revised: added 2's exons by similarity with P. knowleei; signal anchor predicted by SignalP 2.0 HWM (Signal peptide probabilty 0.001, signal anchor probability 0.997) with Pfam match to entry PF00005 ABC_tran, ABC transporter, score 72.50, E-value 9e-18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oin(10596. 10737,11044. 11146,11373. 20416,20578. 20690)
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NKSNEEKKKKLLLDEDELWALNFEKSIKKDIISPIGHDEKSRHNEGMKEEEEDEDDEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Jone="Similarity to P. falciparum elongation factor
1-beta, (AAF27524) (276 aa), fasta scores: opt: 366, E():
11-15, 53.2% identity in 141 aa overlap, revised:
shortened exon 2, splicing confirmed in P. knowlesi; Pfam:
match to PF00736 EFIBD, EF-1 guanine nucleotide exchange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MANTYDELYVPLSYYILQNEGGNTSKIDQANTKKPKKEVINKS
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LCVLNKFKNILITYQLKTIDIYYTYIYIYTLNEKKKLLKNIQDKDIKYLIEIDPLFFLF
FQNFKYFNELNNLLLMKNNFMQPISYNFAYLRDILVRGNENKNIINSTNHDDNPYDIN
                                                                                                                                                                                                                 ODEDDDDDSVDIKYKRHKEKRKSLTTKKYDKKEKHKRKSDHRDXHRRRENHSRHREK
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YKQLFIKFENISLMHLIICSIVSFVLLICILNYIIYYKRKKMMMLNTKYRGKSKSITN
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VIKSPRKVANNYVDGYNVGRI SSHESSINDKKKDNNDNNNDDDNNKNNSVDHIDHLFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="elongation factor 1 (BF-1); putative"
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MYNNHNKYGKYKNNNNNSFYNMRDDTELTDIEENISSKKKKNKFIEKEFSYNTYRNN

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KNNDENDEYGEYDNYDDNMIMSNTSNIMKKKNIKKONIFKTCINFFTTYIKPTLLLKL
                                                                                                                                                                   158 GAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTT 216
                                                                     38 ATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAATTTTTTCTTAAG
                                                                                                                    Gaps
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                       DB 3; Length 253305;
                                              82; Indels
                     Score 47.4; DB Pred. No. 2.7; 1; Mismatches
                      similarity 53.6%;
                                              Conservative
                                            96;
                      Query Match
Best Local
                                              Matches
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Search completed: February 14, 2004, 16:11:49 Job time : 2730 secs

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13 BX404443 9 AL514205 13 BX425020 28 BH137168	13 BX40: 13 BX44(9) ALS14'	13 BX42:	9 AL514 29 CNS0	13 BX44 13 BX42	13 BX42: 14 CB75(13 BX42	29 CNS0	10 BF26 12 BM11 13 BX37	13 BX42 13 BX42 9 AL543 13 BX44	13 BX42	13 BX40	13 BX34	9 AL513	9 AL513	13 BX44	13 BX46 14 CA72	9 AL513:	13 BX40: 9 ALS13	9 AL515	12 BM51, 13 B026	12 BJ44	9 AL514	13 BX44 9 AL514	9 AL514	12 BI74	13 BX44 9 AL513	9 AL514	12 BM52 13 BX42	13 BX42	13 BX40	13 BX41 9 AL515
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ion 5.1.6 04 Compugen Ltd.		(without alignments) 4905.406 Million cell updates/sec	tettogagaggettetgag 529	,	6 residues	choвеп рагаметегв: 45562784		ies 1																predicted by chance to have a	l to the score of the result being printed, of the total score distribution.	RIES		Description		5 AQ803995 HS_2005_A BX424950 BX424950
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 564)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ790276 15.40 B1 F01 MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2240 Col=1 Row=L, genomic survey
                                                                                                                                                                                                                                                                                              121 AAATTATCAAAAGAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCC-TA 179
                                                                                                                                                                                                                                                                                                                    322 TCGGGTATATTTTGGAAGTTGTAAAATACTACGTGTTCTCTTCTAAGTCCCACTCCTCTG 263
                                                                                                                                                                                                                                                     442 TCTTTATACTTTTATTTTATTCCCAAATTTTTATTAAGCAAATATTTCTTTGCTAATCAAT 383
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High Throughput Sequencing Center
High Throughput Sequencing Center
William Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Exa: (206) 616-3887
Email: jwallac@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TCTTTATACTTTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAAT
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                                      Score 481.6; DB 28; Length 515;
Pred. No. 3e-56;
1; Mismatches 5; Indels 1;
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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                                        Query Match 91.0%;
Best Local Similarity 98.6%;
Matches 495; Conservative
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Homo sapiens
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Other GSSs: CIT-HSP-2005M18.TF
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: medadams@tigr.org
Email: medadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13 Reverse
Class: BAC ends.
                 BM547682 AGENCOURT
AL551891 AL551891
BC02523 Home sapi
BC0390979 NISC mq16
AL51532 AL515325
BX415058 BX415058
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BX425800 BX425800
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BX425107 BX46411
BX446411 BX46411
BX46397 BX46397
AL514627 AL514627
BX446397 BX46397
AC5452259 RXCT-23-2
AC549422 ENTDP49TF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 515)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden Ad., K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of a random BAC End Sequence Database for Sequence-Ready Map
Building
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/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .515
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/clone="2005M18"
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BC390979
AL515321
AL515235
BX415058
AL514047
CNS016CW
BX425800
BX425800
BX425107
BX446411
BM06326
BX46411
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COMMENT
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
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BX424950 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA005ZA01
BX424950 mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 AAAAAAACTAAAACAACGCTGAAAAAAGGAAAGTTAGCCCCTATCGGGTATATTTTGGA 334
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                                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Seq primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 AAGAGAAAGCAGTCACCCTCTTCCATGACAACAACCCATGACGGGTGCTTGCCTTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 AAAGAAAGCAGTCACCTCTTCCATGACAACAACCATGACCGGCTGCTTGCCTGCT
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                                                                   Sequence-tagged connectors: A sequence approach to mapping and
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 69.7%; Score 368.6; DB 28; Length Best Local Similarity 95.9%; Pred. No. 7.4e-41; Matches 377; Conservative 1; Mismatches 15; Indels
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Location/Qualifiers
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195 bp DNA linear GSS 09-AUG-1999
HS_2005_A2_G09_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2005 Col=18 Row=M, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 GGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAATTTTTCTTAAGCAAATAT 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAGTGACGCACACTCAAGCTGTTCGGGGACTTCCAGAATAAACCAAAACCAGCTGTATTA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 CTGGTCTTTGACATCCTCTCTGGTCAGGG--CCAAGTCACTGTCCCTGTCTTGGAGAGGG 521
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 395)
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                                                                                                                                                                                                                                            /clone lib-"CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 GGTGATTATGCTTCCTTCTTTATACTTTTTATTGATTCCCAAATTTTTTAAGCAGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          504 TICTITICCTAATCAATAAATTATCAAAAGAATTAAAAAACTGAGAGGAACGCTTGAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 GGAAAGTTAG-CCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 GACAACACCATGACCGGCTGCTTGCGTGCTCCATCACAGGAGGTGCAGCAGAGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITCTICCCAGGGIIGIGGGCACCTIGAACIAICCIGGCTIGCIAGCIAAGAAACIGCCC
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                                                                                                                                                                                                                                                                                                                                                                  82.1%; Score 434.2; DB 28; Length 564; 95.7%; Pred. No. 7.8e-50; ive 1; Mismatches 17; Indels 3;
  BAC end Web Server: http://www.htsc.washington.edu
Plate: 2240 row: L column: 1
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 564.
                                                                                                                                                                                                                                                                                                             31 others
                                                                                                                       1. :564
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="texon:9606"
/clone="Plate=2240 Col=1 Row=L"
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                                                                                                                                                                                                                              /sex="male"
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Matches 465; Conservative
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                                                                                                                                                                                            Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6403.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq-CLOBA005ZA01FP1&cluster=6403.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA005ZA01FP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
399 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  695 AAAWTIWWRRRRRRRRRRRRRRRRRRRRRRRRRRRRRTITIKKITKKICIAWDDNW 754
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1091)
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 CACTCCTCTGTTTTCTTTGAGCAGGAAAGAGGAAAGCAGTCACCCTCTCTTCCA 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.3%; Score 60; DB 13; Length 1091; 30.5%; Pred. No. 32; tive 74; Mismatches 88; Indels
                                                                                                                                     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .1091
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:966"
/clone="CLOBA005ZA01"
GI:30770416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX404443.1 GI:30635181
                                        Homo sapiens (human)
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Best Local Similarity 30.5.
Best Ti, Conservative
                                                              Homo sapiens
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Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 9106 EVRY cedex - France
BP 191 9106 EVRY cedex - France
BP 191 9106 EVRY cedex - France
BP 191 9106 EVRY cedex - France
BP 191 9106 EVRY cedex - France
BP 191 9106 EVRY cedex - France
Introper This sequence belongs to sequence cluster 6537.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CL0BB029ZG02FP1kcluster=6537.f. Contact :
From Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BB029ZG02FP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="NEUROBLASTOMA"
/cione lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT_6; lst strand cDNA was primed
with a NotI-ollygo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
13 g 326 t 194 others
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1. (bases 1 to 770)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished

On Feb 13, 2001 this sequence version replaced gi:12777699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 WKTTTTKTTGGGGGTTTWWAAAAAATTTTTTTTTTTTTWWTAAAATTRGGAAAAA 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 միրրերդորդորդորդորդորդորդորդորդորդորդուրդորդորդորդորդորդուրդորդու
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CLOBBO062G12 3-PRIME, mRNA sequence.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
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Live 18; Mismatches 108; Indels
Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
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Homo sapiens
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/clone="CL0BA007ZD06"
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Invitrogen. This sequence belongs to sequence cluster 6437.r For more information about this cluster, see
    http://www.genoscope.cnm.fr/
    cgi-bin/cluster.cgi?seq=CL0BB006ZG12FP1&cluster=6437.r. Contact :
    Feng Liang Email : filang@lifetech.com URL:
    http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
    Faraday Avenue Genoscope sequence ID : CLOBB006ZG12FP1.
    Location/Qualifiers
    ir. 770
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    /norganism="Homo sapiens"
    /norganism="Homo sapiens NEUROBIASTOMA"
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    /tlone="CLOBB006ZG12"
    /tlone="CLOBB006ZG12"
    /tlone="Vactor: pCMYSDORT 6; lat strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into I and cloned into I and EDORV sites of the pCMVSPORT 6 vector.
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BX452020 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA0072D06
BX425020
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Genoscor. General National de Sequencage
BP 191 91006 EVRY cedex - France
BR 181 sequeséquencacope.cna.fr, Web : www.genoscope.cna.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8225.r For
more information about this cluster, see
http://www.genoscope.cna.fr/
cgi-bin/cluster.cgi?seq=CLOBA007ZD06FP1&cluster=8225.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://tulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA007ZD06FP1.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 252)

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                                                                                                                                                                                                                                                                                                                                                                                                                                               145 others
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/mol_type="mRNA"
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Contact: Genoscope
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Matches 77; (
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/tissue type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
1 20 2 24 89 t 35 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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ENTOK14TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD. 20850,
Fax: 301 838 9363
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47.9%; Pred. No. 3.2e+02;
tive 23; Mismatches 63
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Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 894)
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BH137168
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High quality sequence stop: 522.
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Matches 79, Conservative
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double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized." 88 others
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefegenoscope.ons.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBA002ZH05FP1.
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                            m.
              whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and Barell, Oxford University Press, 1999)."
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                                                                                                    10.3%; Score 54.6; DB 28; Length 894; 52.9%; Pred. No. 1.9e+02;
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                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                247
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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                                                                                                                                 0; Mismatches 104;
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H.O. and Venter, J.C.
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Mammalia; Butheria; Primates;
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147 AAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAAT 206
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li (bases 1 to 1201)
Li W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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Genoscope - Centrer National de Sequencage
Genoscope - Centrer National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : filang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avanue Genoscope sequence ID : XCLOBB001ZA03FP1.

Location/Qualifiers
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Contact: Genoscope
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Contact: Genoscope
Benoscope - Centre
Benoscope. Contact
Benoscope. Cons. fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9703.f For
                                                                                                                                              Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 817.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                             http://www.genoscope.cns.fr/
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cgi-bin/cluster.cgi?eeq=CLOBA007ZH01FP1&cluster=817.f. Contact
Feng Liang Email : filang@lifetech.com NRL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA007ZH01FP1.
Location/Qualifiers
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  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                  1 (bases 1 to 1162)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
Library was not normalized."
24 c 24 g 102 t 24 others
                                            AL514791 Sof bp mRNA linear EST 08-MAY-2003 AL514791 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone CLOBB015ZE10 3-PRIME, mRNA sequence.
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3-FRIME, mRNA sequence.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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BP 191 91006 EVRY cedex - France
Bmalis sequenceope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1606.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BB015ZE10FP1&cluster=1606.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BB015ZE10FP1.
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                                                                                                                         AL514791
AL514791.2 GI:30464676
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                                                                                                                                                                                                                              Homo sapiens
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RESULT 11
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255 131

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/tissue_type="PLACENTA"
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/clone_lib="Homo sapiens PLACENTA"
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
198 others
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with a NotI-olig(MI) primer. Five prime end enriched,
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the Not I and ECORV sites of the pCMVSPORT 6 vector.
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3-PRIME, MENA sequence.
BX425020
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 252)

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                                                                                                                                                                                                                                                                                                                                                                                                     72 TTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAA
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8225.r F
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBA007ZD06FPl&cluster=8225.r. Contac
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA007ZD06FPl.
Location/Qualifiers
                                                                                                                                                                                                                                                                                     10.0%; Score 52.8; DB 9; Length 1104; 36.7%; Pred. No. 3e+02; Live 46; Mismatches 54; Indels 0;
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BP 191 91006 EVRY cedex - France
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/clone="CL0BA009ZF09"
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                                                                                                                                                                                                                                                                                                                                                     58; Conservative
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/clone lib="Homo sapiens PLACENTA"
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
16 26 others
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AL513809 Homo sapiens PLACENTA Homo sapiens cDNA clone CL0BA009ZF09
3-PRIME, mRNA sequence.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
I (bases I to 1104)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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cgi-bin/cluster.cgi?seq=CLOBA009ZF09FPl&cluster=1095.f. Contact
cgi-bin/cluster.cgi?seq=CLOBA009ZF09FPl&cluster=1095.f. Contact
Feng Liang Bmail: fliang@lifetech.com/NL:
http://fulllength.invitrogen.com/InvitroGen Corporation 1600
http://fulllength.invitrogen.com/ invitroGen Corporation 1600
Faraday Avenu Genoscope sequence ID: CLOBA009ZF09FPI.
Location/Qualifiers
                   http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?eeq=CLOBA011ZH06FP1&cluster=9703.f. Contact
cgi-bin/cluster.cgi?eeq=CLOBA011ZH06FP1&cluster=9703.f. Contact
Feng Liang Email : fliang@lifetech.com WLL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA011ZH06FP1.
Location/Qualifiers
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more information about this cluster, see
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/db_xref="taxon:9606"
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Drosophila melanogaster genome survey sequence SP6 end of BAC BACNISHO of DrosBAC library from Drosophila melanogaster (fruit AL106008 AL106008 IG:5619558
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Determination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a thitp://www.edgp.ebi.ac.uk - This Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 GAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCCTATCGGGTATATTTTGGAAGTTGTAAA 204
                                                        146 AAAGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 TACTACRIGITCICTICIAAGICCCACICCICIGITTTCITTGAGCAGGAAAGAGAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1203)
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                                                                                                    205 ATACTACRIGITCTCTTCTAAGTCCCACTCCT 236
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                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
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/db_xref="taxon:7227"
/clone="akcN15E10"
/clone lib="brosBAC"
/plasmId="pBeloBAC11"
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/clone_lib="Homo sapiens NEUROBLASTOWA"
/note="Vector: pcMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoNY sites of the pcMVSPORT 6 vector.
Library was not normalized.
177 others
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (basea 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Pull-length cDNA libraries and normalization
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BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7847.r For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgirsqc-CL0BB010ZG01FP1&cluster=7847.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BB010ZG01FP1.
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                                                                              27 TTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTTTTCCCAAA
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                                        Gaps
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AL514421 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CLOBB010ZG01 3-PRIME, mRNA sequence.
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Contact: Genoscope
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46.2%; Pred. No. 3.3e+02;
ive 12; Mismatches 102; Indels
             6.8e+02;
ches 51; Indels
                                      Mismatches
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/db_xref="taxon:9606"
/clone="CLOBB010ZG01"
               Pred. No.
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49.0%; ELL.
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Matches 98; Conservative
                                   70; Conservative
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                 Best Local Similarity
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/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pcWVSPORT_6" ist strand cDNA was primed
/note="vector: pcWVSPORT_6" ist strand cDNA was digested with not I and cloned,
double-strand cDNA was digested with Not I and cloned into
the Not I and Ecotv sites of the pcWVSPORT 6 vector.
Library was not normalized."
191 g 116 t 194 others
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BP 191 91006 EVRY cedax - France
BB 191 91006 EVRY cedax - France
BB 191 91006 EVRY cedax - France
BB 191 91006 EVRY cedax - France
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : XCLOBB001ZA03FP1.

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6437.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 TTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTATTCCCAAA
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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31.5%; Pred. No. 3.5e+02;
tive 55; Mismatches 43; Indels 0;
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                               1 (Dases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLOBB012ZG07 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="XCL0BB001ZA03"
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BX425394.1 GI:30788457
                        (bases 1 to 1201)
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                                                                                                                   Contact: Genoscope
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//mol type="manny" mol type="manny" mol type="manny"
/clone=lib="Homo sapiens PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMYSPORT 6; lst strand cDNA was primed
with a Not1-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

234 others
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                                                                                                                                                              EST 13-MAY-2003
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Bp 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: XCLOBA001ZE02FP1.
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Li, W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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1201 bp mRNA linear EST 15-W
BX446296 Homo sapiens OEUROBLASTOWA Homo sapiens CDNA clone
XCLOBB001ZA03 3-PRIME, mRNA sequence.
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0
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BX424825 Homo sapiens PLACENTA Homo sapiens cDNA clone
XCLOBA001ZE02 3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.9%; Score 52.2; DB 13
33.1%; Pred. No. 4.6e+02;
                        854 WMCCACYCGBCCCCCYYYTAYTATCSGSS 825
326 AAGGTGCAGCAGAGCCCTTTTCTTCCCAGG 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 AAGCAACGCTTGAAAAAGGAAA 169
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                                                                                                                                                                                                                                                        BX424825.1 GI:30647817
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                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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Best Local Similarity
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JOURNAL
COMMENT
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AUTHORS
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BX446296
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EST 15-MAY-2003

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the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
140 c 113 g 196 t 105 others
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Xenopus laevis
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/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6877304"
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                                                                                                       ch 9.8%;
1 Similarity 53.6%;
98; Conservative
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                                              369
                                                                                                          Query Match
Best Local
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CB756565
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                                                                                                                                        /tissue type="NEERON BLASTOMA"
/clone lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pcm/vsporm for late strand cDNA was primed
with a NotI-ollgo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized."

184 c 192 g 142 t 188 others
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/clone lib="Homo sapiens NEUROBLASTOWA"
/note="Vector: pGr/VSORI & ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.1
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 923)

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BP 191 91006 EVRY cedex - France
Bmall: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4504.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BB012ZH03FP1&cluster=4504.f. Contact
cgi-bin/cluster.cgi?seq=CL0BB012ZH03FP1&cluster=4504.f. Contact
Feng Liang Email : filangellfetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BB012ZH03FP1.
Location/Qualifiers
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BX425397 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone CLOBB012ZH03 3-PRIME, mRNA sequence.
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Faraday Avenue Genoscope sequence ID : CL0BB012ZG07FP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                       62; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                        Query Match
9.8%; Score 52; DB 13;
Best Local Similarity 50.6%; Pred. No. 4.2e+02;
Matches 80; Conservative 16; Mismatches 62,
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                             /organism="Homo sapiens"
                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL0BB012ZG07"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
I (bases 1 to 964)
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Sequenced with vector primer
Contact: Robert Drimer
Tissue Procurement: Drs. Donald Brown and Liquan Cai
cDNA Library Preparation: CLONTECH
CDNA Library Preparation: CLONTECH
CDNA Library Preparation: CLONTECH
CDNA Library Preparation: CLONTECH
CDNA Library Preparation: CLONTECH
CDNA Library Preparation: CLONTECH
CDNA Library Preparation: CLONTECH
CDNA Library Preparation: OF Sequence distribution information can be
found through the I.M.A.G.E. Consortium/LLN at:
http://image.llnl.gov
Plate: LLCM3115 row: 1 column: 07
High quality sequence stop: 158.
Location/Qualifiers

I. : :64
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/clone lib="NICHD XGC Tad1"
/note="Organ: Developing Tadpole, Vector: pDNR-LIB;
/note="Organ: Developing Tadpole, Vector: pDNR-LIB;
Site 1: Sfi; Site 2: Sfi; 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:
S'-CAGGGCCATATGGGC-3' and 3' adaptor sequence:
C. or G and N = A, C, G, or T). Average insert size 1.6 kb
/range 0.9-3.0 kb). 15/15 colonise contained inserts by
/range 0.9-3.0 kb). 15/15 colonise contained inserts by
/range 0.9-3.0 kb). Lis/15 colonise and
was constructed by Clontech Laboratories (Palo Alto, CA)."
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                                                                                                                                                                                                                                                                                                                                                                  146 AAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAA 205
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                                                                                                                                                                                                                                                                                                                  26 ATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTCCCAA
                                                                                0; Gaps
        DB 13; Length 923;
Score 51.8; DB 13; Length Pred. No. 4.5e+02; 4; Mismatches 81; Indels
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CNS0301Z 589 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 043121 of library G from Tetraodon nigroviridis, genomic survey
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodon.
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                      62 CITIAIACTITIAITATTCCCAAAITTTTTTTTTAAGCAAAIATTTCTTTGCTAATCAATA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rocest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Sautin, W., Bernot, A. and Weissenbach, O. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetracdon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Genoscope sequence ID : C0BG043AE11LP1~end : T7" 20 c 38 g 98 t 55 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
NAT. Genet. 25 (2), 235-238 (2000)
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Length 589;
                                                                                                   Indels
                                                              123 ATTATCAAAAGAAAAAAAAACTGAAAGCAACGCTTGAAAAAAAGGAAA
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/organism="Tetraodon nigroviridis"
/orl_type="genomic DNA"
/db_xref="faxon:99883"
/clone="043121"
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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    (bases 1 to 589)
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Matches 92
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/clone lib="Homos sapiens PLACENTA"

/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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BX424931 Homo sapiens PLACENTA Homo sapiens cDNA clone CL0BA004ZC11
3-PRIME, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 512)
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BP 191 91006 EVRY cedex - France
Bmail: sequefegenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1009.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BA004ZC11FP1&cluster=1009.f. Contact:
from Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CL0BA004ZC11FP1.
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                                                                964;
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49.1%; Pred. No. 6.9e+02;
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                                                                51.6; DB 14;
No. 4.7e+02;
                                                                                                       0; Mismatches
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/clone="CL0BA004ZC11"
                                                                Score Pred. 1
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                                                                9.8%;
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                                                                                                     96; Conservative
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1. (bases 1 to 738)
1.4, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Ombublished
On Reb 13, 2001 this sequence version replaced gi:12777401.
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRAIl: SequenceCope.cns.fr, web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9836.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
egi-bin/cluster.cgi?seq=CLOBA006ZC11FP1&cluster=9836.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA006ZC11FP1.
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52.0%; Pred. No. 6.1e+02;
ive 14; Mismatches 57; Indels
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                                                                                                                      Query Match
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ORIGIN
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                                                                     BASE COUNT
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VERSION
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SOURCE
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TITLE
JOURNAL
COMMENT
                                                                                                                                                     Matches
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BX371218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
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                                                                                       ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="NIA Mouse Newborn Brain cDNA Library" //clone lib="NIA Mouse Newborn Brain; Vector: pSPORT1 (Invitrogen); Site_1: Sali; Site_2: Noti, Mouse cDNA project by the Laboracory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgun.grc.nia.nih.gov/cDNA). Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                        BM115165 856 bp mRNA linear EST 30-JAN-2002 L0816E08-3 NIA Mouse Newborn Brain cDNA Library Mus musculus cDNA clone L0816E08 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mummalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Sases 1 to 856)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Pantano, S., Lim, M.K.
and Ko, M.S.H.
                                                                                                                                                                                                                                     66
                                                                     40 TTAIGGGIGAITITIGCTICCTICITIAIACTITITAITCCCAAAITITITICTIAAGCA
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Genetice Maintenant Institutes of Health National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdns@lgsun.grc.nia.nih.gov
Plate: L0816 row: E column: 08
Seg primer: -21M13 Forward
High quality sequence stop: 856
POLXA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Systematic Analyses of NIA Mouse Newborn Brain cDNA Library
Unpublished
                                    ;
0
   Length 838;
                                    Indels
Score 51.2; DB 10;
Pred. No. 5.7e+02;
1; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Newborn Brain"
/dev_stage="Newborn"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | db xref="niaEST:L0816E08-3"
| db xref="taxon:10090"
| clone="L0816E08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM115165.1 GI:17078183
                    53.7%;
Query Match
Best Local Similarity 53.7°
Matches 101, Conservative
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                                                                                                                                                                                                                                                                       220 TTCTAAGT 227
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BM115165
LOCUS
DEFINITION
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VERSION
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COMMENT
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SOURCE
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Bp 19 91006 EVRY cedex - France
Bmail: seqrefégenoscope.ns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 355.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi'seq=CSOBAHO16ZE09FM1&cluster=355.r. Contact :
Feng Liang Email : fliang@alifetech.com URL :
Feng Liang Email : fliang@alifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAHO16ZE09FM1.
plasmid vector. The DH10B E. Coli host was trassiformed with ligation mixture by the standard chemical method. The worstage insert size is about 1.9 kb. The library was constructed by the library was constructed by 242 t 71 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 TATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 AAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="CSOD7067114"
/cell type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fincte="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWSPORT ecctr. Library was normalized."

113 c 114 g 173 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 927)
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                                                                                                                                                                                                                                                                                                                                                                                     17 ICGIGGCIGATITATATGCTGATITATGGGTGATITIGCTTCCTTCTTTATATTTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                          9.7%; Score 51.2; DB 12; Length 856; 42.2%; Pred. No. 5.6e+02; ive 0; Mismatches 126; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 927)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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/mol_type="mRNA"
/db xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                  92; Conservative
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us-10-027-632-1.rst

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/tissue type="NEUROBLASTOWA"
/clone lib="Homo sapiens NEUROBLASTOWA"
/clone lib="Homo sapiens NEUROBLASTOWA"
/clone lib="Homo sapiens NEUROBLASTOWA"
/clone lib="Vector: pcw/SPORT 6; lst strand cDNA was primed
/with a NotI-oligo(dT) primer. Five prime end enriched,
/double-strand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
Library was not normalized."
89 others
                                                                                                                                                                                                                                            BX425197

381 bp mRNA linear EST 15-MAY-2003
BX425197 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 12-MAY-2003
      AAATATTICTITGCIAATGAATAAATTATCAAAAGAAAAAAACTGAAAGCAAGGCITG 158
                               71 TITATITATICCCAAATTITICTTAAGCAAATATTICTTIGCTAATCAATAAATTATCAA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 381)

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BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6437.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBB003ZH07FPl&cluster=6437.r. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBB003ZH07FPl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 CIGIAGICGIGGCIGATITATATGCIGATITATGGGIGATITIGCITCCTICTITATACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 381)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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/db_xref="taxon:9606"
/clone="CL0BB003ZH07"
                                                                                                                                                                                                                                                                                                                               BX425197.1 GI:30769941
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63; Conservative
                                                                                                                                  189 AAAAAAAAAAA 199
                                                                                            159 AAAAAAGGAAA
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BX425197/c
LOCUS
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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ALS43011
LOCUS
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KEYWORDS
SOURCE
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/clone lib="Homo sapiens PLACENTA"
/clone lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
1 9 72 t 26 others
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRMA11: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9703.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgl?seq=CL0BA011ZH06FP1&cluster=9703.f. Contact:
Feng Liang BRMA1: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CL0BA011ZH06FP1.
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234 bp mRNA linear EST 15-MAY-2003
BX425129 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA011ZH06
                                                                                                                                  135
                                                                                                                                                                        TITIAITITATICCCAAAITITICITAAGCAAAIAITICTITGCIAATCAAIAAATTATCA 129
                                                                                                                                                                                                                     195
                                                                                                                                                                                                                                                           AAAGAAAAAAAACCTGAAAGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATAT 189
                                                                                                                                                                                                                                                                                                        255
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                                                 Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 234)
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9.6%; Score 50.8; DB 13; Length 927;
53.5%; Pred. No. 6.1e+02;
iive 0; Mismatches 92; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .234
/organiem="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="CLOBA011ZH06"
                                                                                                                                                                                                                                                                                                                                                 TITGGAAGITGIAAAIA 207
                                                                                                                                                                                                                                                                                                                                                                                            TTTAAAAAAAAAAAAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-PRIME, mRNA sequence.
BX425129
BX425129.1 GI:30780435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens (human)
                      Best Local Similarity 53.5
Matches 106; Conservative
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Best Local S
    Query Match
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                                                                                                                                                                                                                                            On Feb 15, 2001 this sequence version replaced gi:12875489.
On Feb 15, 2001 this sequence version replaced gi:12875489.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@qenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9876.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODE013DF11QP1&cluster=9876.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODE013DF11QP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="CSODE013YL22"
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Library was not normalized."
158 c 203 g 237 t 62 others
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BX446492 Homo sapiens PLACENTA Homo sapiens cDNA clone CL0BA009ZC08
3-PRIME, mRNA sequence.
AL543011 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE013YL225-PRIME, mRNA sequence.
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1. (bases 1 to 894)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Pull-length cDNA libraries and normalization
Unpublished
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11.5%; Pred. No. 6.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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                                                         AL543011.2 GI:30548727
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871 ATTWAAKAWTTTTT 885
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                                                                                               Homo sapiens (human)
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Matches 81; Conserv
                                         AL543011
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/clone_lib="Homo sapiens PLACENTA"
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 332)
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                                                                                                                                                                                                         Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Brail: seqref@genoscope.cns.fr
http://www.genoscope.cns.fr/
cgi-bin/Cluster.cgi?seq=CLOBA0092C08FP1&cluster=6609.f. Contact :
Frog Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA0092C08FP1.
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BP 191 91006 EVRY cedax - France
Bmail: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6437.r For
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BX425197 Homo sapiens NEUROBLASTOWA Homo sapiens cDNA clone
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Lull-length cDNA libraries and normalization
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Homo sapiens
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                                                                                                                                                           Unpublished
Contact: Genoscope
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Contact: Genoscope
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Gaps

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/note="Vector: pcWVSPORT 6; lst strand cDNA was primed
/note="Vector: pcWVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
Library was not normalized."
115 c 106 g 188 t 138 others
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AL513975 Homo sapiens PLACENTA Homo sapiens cDNA clone CL0BA011ZE10
3-PRIME, mRNA sequence.
AL513975.2 GI:30463860
                                                                                                                                                                                                                                                                                                                                                                                                                                27 ITTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATATTCCCAAA
                                                                                                                                                                                                                                                                                                                                                  Length 940;
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                                                                                                                                                                                                                                                             54; Indels
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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                                                                                                                                                                                                                  Score 50.4; DB 13
Pred. No. 6.9e+02;
3; Mismatches 54
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                                                                                                                                                                                                                  ch 9.5%;
1 Similarity 58.7%;
81; Conservative
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Homo sapiens
                                                                                                                                                        393
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Best Local &
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                                                                                                                                                      BASE COUNT
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                                                                                                                                               1. .381
| / organism="Homo sapiens" | / organism="Homo sapiens" | / organism="Homo sapiens" | / do xref="texton:9606" | / clone="CL0BB003ZH07" | / clone="CL0BB003ZH07" | / clone="type="NEUROBIASTOWA" | / clone lib="type="NEUROBIASTOWA" | / note="Vector: pCWV8PORT 6; lst strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized." | 89 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Genoecope

Contact: Genoecope

Genoecope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

BP 191 91006 EVRY cedex - France

Email: seqrefégenoscope.ns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 1357.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=Ci0BB027ZB08FPl&cluster=1357.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitroden Corporation 1600

Faraday Avenue Genoscope sequence ID : CL0BB027ZB08FPl.
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                    http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BB003ZH07FPl&cluster=6437.r. Contact
cgi-bin/cluster.cgi?seq=CL0BB003ZH07FPl&cluster=6437.r. Contact
Feng Liang Email : fliang@lifetech.com/RL.
http://fulllength.invitrogen.com/InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BB003ZH07FPl.
Location/Qualifiers
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more information about this cluster, see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/tissue type="PLACENTA"
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the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7629.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBA011ZE10FP1&cluster=7629.r. Contact :
Feng Liang Email : fliangelifeech.com UEL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA011ZE10FP1.
                                                                                                                                                                                                    Unpublished
On Feb 13, 2001 this sequence version replaced gi:12777469.
Contact: Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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206 AAAAAAAAAAAAAAAAAAAAAAA 184
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                                                                                                                                             3-PRIME, mRNA sequence.
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Best Local Similarity 51.04
Matches 73; Conservative
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Contact: Genoscope
Genoscope - Centre National de Sequencage
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BP 19106 EVRY cedex - France
BP 19106 EVRY cedex - France
BP 19106 EVRY cedex - France
BP 19106 EVRY cedex - France
BP 19106 EVRY cedex - France
BP 19106 EVRY cedex - France
Email: sequence belongs to sequence cluster 7985.fr
Invitrogan. This sequence belongs to sequence cluster 7985.fr For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CiubBB015ZCloFP1ccluster=7985.f. Contact :
Fong Liang Email: fliang@lifetech.com URL :
Fong Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBB015ZClOFP1.
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Library was not normalized."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 375)

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. 6.1e+02;
tches 55;
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                                                        24 TGATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCT
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                      19; Mismatches
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       Pred. No.
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   49.38;
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                      72; Conservative
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Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
     Best Local Similarity
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1024 bp mRNA linear EST 05-MAY-2003
BX349610 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI021YP19 3-PRIME, mRNA sequence.
BX349610.1 GI:30365363
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 661)
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BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 108.r For
more information about this cluster, see
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cgi-bin/cluster.cgi?seq=CLOBA011ZG02FP1&cluster=108.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA011ZG02FP1.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12777509.
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51.0%; Pred. No. 8.8e+02;
ive 16; Mismatches 54; Indels (
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/organism="Homo sapiens"
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3-PRIME, MRNA sequence.
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1 (bases 1 to 1126)
1 (Aruber, C., Jessee, J. and Polayes, D. Full.length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96
                                                  Euteleostomi;
                                                                                                                                                                                                    Email: seqref@genoscope.ons.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7295.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAHO13ZGO4FM1&cluster=7295.f. Contact
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAHO13ZGO4FM1.
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCWYSORT 6 vector. Library was normalized.
79 c 53 g 378 t 30thers
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segreí@genoscope.cns.fr
                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                 1 (bases 1 to 1024)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
                                                                                                                                                     Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI021YP19"
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                  sapiens (human)
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/tissue type="PLACERTA"
/clone lib="Homo sapiens PLACERTA"
/note="Vector: pCWVSPORT 6; lst strand cDNA was primed
/note="Vector: pCWVSPORT 6; lst strand cDNA was primed
/with a VotI-oligo(dT) primer. Flve prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
143 c 36 g 250 t 208 others
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AL513719 Homo sapiens PLACENTA Homo sapiens cDNA clone CLOBA007ZH01
3-PRIME, mRNA sequence.
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                                                                                                     http://www.genoscope.cns.fr/
ggl-bin/cluster.cg1?seq=ClDBA004ZG10FP1&cluster=2672.f. Contact :
ggl-bin/cluster.cg1?seq=ClDBA004ZG10FP1&cluster=2672.f. Contact :
Feng Liang Email : fliangelifecech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA004ZG10FP1.
Location/Qualifiers
1. 1126
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1162)
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 2672.f For more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 817.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBA007ZH01FP1&cluster=817.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA007ZH01FP1.
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Liw. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12777213.
Genoscope - Centre National de Sequencage
Genoscope - Centre National - France
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Pred. No. 6.7e+02;
8; Mismatches 56
                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBA004ZG10"
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Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 1919 19106E EWRY cedex - France
BP 1919 19106E EWRY cedex - France
BRail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1731.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=XCLOBB001ZE02FP1&cluster=1731.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : XCLOBB001ZE02FP1.
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/clone lib="Homo sapiens NEUROBLASTOWA"
/clone lib="Homo sapiens NEUROBLASTOWA"
/clone lib="Homo sapiens NEUROBLASTOWA"
//tote="Vector: pCWVSPORT 6; lst strand cDNA was primed
/with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
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                                                                                                                                                                                                                                                                          125 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTWAACSCAAATTTKTTTTTATTWAAAGGR 184
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1201)

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                                                                                                                                                                                                                                                                                                                        122 AATTATCAAAAGAAAAAAACTGAAAGCAACGCTTGAAAAAAAGGAAAG 170
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53.1%; Pred. No. 6.5e+02;
ive 12; Mismatchés 55; Indels 0;
                                        Length 1189;
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                                        Score 50.2; DB 9;
Pred. No. 6.5e+02;
9; Mismatches 72;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="XCL0BB001ZE02"
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                                        9.5%;
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On Feb 13, 2
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/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
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the Not I and EcoNP as of the pCMVSPORT 6 vector.
Library was not normalized."
226 c 199 g 222 t 208 others
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/cissue type="PLACENTA"
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/note="Vector: pcMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoNA wites of the pcMVSPORT 6 vector. Library was not normalized."
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1 (Dases 1 to 1189)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRmall: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1883.f For-
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.gi?seq=CLOBA009ZB08FPL&cluster=1883.f. Contact :
Feng Liang-Email : filang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitrogen.corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                             27 TTTATATGCTGATTTTATGGGTGATTTTTGCTTCCTTCTTTATACTTTTATTTTATTCCCAAA
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                Length 1162;
                                                                                                                                                                                                                               298 others
                                                                                                                                                                                                                                                                                                ch 9.5%; Score 50.2; DB 9; Length 1
1 Similarity 38.5%; Pred. No. 6.6e+02;
55; Conservative 40; Mismatches 48; Indels
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                   /db_xref="taxon:9606"
/clone="CL0BA007ZH01"
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/close type="PLACENTA"
/close lib="Homo sapiens PLACENTA"
/close lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSDORT 6; 1st strand cDNA was primed
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double-strand cDNA was digested with Not I and cloned into
the Not I and Ecorv sites of the pCMVSPORT 6 vector.
Library was not normalized."
18 c 19 g 130 t 27 others
                                                                        294 bp mRNA linear EST 22-MAY-2003
BX446415 Homo sapiens PLACENTA Homo sapiens cDNA clone CL0BA005ZH05
3-PRIME, mRNA sequence.
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BP 191 91006 EVRY cedex - Prance
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BP 191 91006 EVRY cedex - Prance
BP 191 91006 EVRY cedex - Prance
BP 191 91006 EVRY cedex - Prance
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5229.r For
http://www.genoscope.org.fr/
cgi-bin/cluster.cgi?seq=CLOBA005ZH05FP1&cluster=5229.r. Contact ::
Feng Liang Email : fliangaliferech.com URL :
http://tulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA005ZH05FP1.
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 294)
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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/mol_type="mRNA"
/db_xref="taxon:9606"
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BX446274/c
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BP 191 91006 EVEY cedex - FRANCE (B-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Betermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster and these BACs inbrary was prepared by Kazutoryo Oscogawa and Aaron Mammoser in Piteter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland REY library and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers

Location/Qualifiers

Location/Qualifiers
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TITIGCTICCTICITIATACTITIATITCCCAAATITITICTIAAGCAAATATITICTI 109
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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9.5%; Score 50; DB 29; Length 928;
Best Local Similarity 31.3%; Pred. No. 7.9e+02;
Matches 62; Conservative 59; Mismatches 77; Indels
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/mol_type="genomic DNA"
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/note="end : T7"
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1769.f For
more informantion about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seqaxCLOBA0012B11FP1&cluster=1769.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : XCLOBA001ZB11FP1.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Primates, Catarrhini, Hominidae, Homo.
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                         Mammalia; Eutheria; Primates; Catarrhini; Hor
1. (bases 1 to 314)
Li W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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Search completed: February 14, 2004, 16:55:33 Job time : 2632 secs

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Sequence 81169, A
Sequence 81169, A
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Sequence 81416, Ap
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| Cgn2_6/ptodata1/pubpna/USO7_PUBCOMB.seq:*
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| Cgn2_6/ptodata1/pubpna/USO9_PUBCOMB.seq:*
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US-10-027-632-300106

US-09-814-352-1318

US-09-814-352-11218

US-09-814-353-1169

US-09-814-353-1169

US-09-814-353-1169

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US-09-814-353-1169
                                                                                                                                                hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 100 summaries
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                                    nucleic search, using sw model
                                                                                                            IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Sequence 8192, Apple Sequence 11165, A Sequence 11165, A Sequence 11165, A Sequence 17782, A Sequence 17782, A Sequence 17782, A Sequence 1782, A Sequence 1781, Apple Sequence 1881, Apple Sequence 1

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Sequence 141, App Sequence 1580, Ap Sequence 146, App Sequence 257, App Sequence 4844, App Sequence 1141, A

US-09-770-445-141 US-10-311-455-1580 US-10-240-453-146 US-10-240-453-146 US-09-814-353-4844 US-09-814-353-11141 US-09-814-353-11163 US-09-814-353-11169 US-09-814-353-11169

US-10-312-841-2 US-10-1198-846-9603 US-09-814-353-6142 US-09-814-353-6142 US-09-814-353-12421 US-09-814-353-27670 US-09-814-353-2534 US-10-027-632-118342 US-10-027-632-118342 US-10-027-632-118343 US-10-027-632-118343 US-10-027-632-118343 US-10-027-632-118343 US-10-027-632-118343 US-10-027-632-118343 US-09-960-352-12673 US-09-814-353-11622 US-09-814-353-11622 US-09-814-353-11635 US-09-814-353-11635 US-09-814-353-11639 US-09-814-353-11395 US-09-814-353-11395 US-09-814-353-11395 US-09-814-353-11395 US-09-814-353-11395 US-09-814-353-11395 US-09-814-353-11395 US-09-814-353-11395

Sequence 11169, A Sequence 2303, Ap

Sequence

Qy 301 GGCTGCTTGCCTGCTCCATCACAGGAAGGTGCAGCACAGAGCTTTTCTTCCCAGGGTTGT 360 l	Oy 481 CTCTGGTCAGGCCAAGTCACTCTCCTGTCTTCGAGAGGCTTCTGAG 529 Db 481 CTCTGGTCAGGCCAAGTCACTGTCCCTGTCTTGGAGAGCTTCTGAG 529	RESULT 2 US-10-027-612-1 US-10-027-612-1 Sequence 1, Application US/10027632 Sequence 1, Application US/10027632 Sequence 1, Application US/10027632 APPLICANT: Wang, David G TITLE OF INVENTION: Delymorphisms in the Human Genome FILE REFERENCE: 108927.129 CURRENT APPLICATION NUMBER: US/10/027,632 CURRENT APPLICATION NUMBER: US 60/18,006 PRIOR APPLICATION NUMBER: US 60/18,006 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR APPLICATION NUMBER: US 60/198,676 PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR PILING DATE: 2000-03-29 PRIOR PILING DATE: 2000-03-29 PRIOR PELING DATE: 1999-11-23 PRIOR APPLICATION NUMBER: US 60/165,358 PRIOR PELING DATE: 1999-01-23 PRIOR PELING DATE: 1999-09-28 PRIOR PILING DATE: 1999-09-09 PRIOR FILING DATE: 1999-09-09 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1 LENGTH: 529 TTPE: DATA CREATION: Human US-10-027-632-1	Query Match 99.9%; Score 528.6; DB 14; Length 529; Best Local Similarity 100.0%; Pred. No. 1.5e-119; Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 CATGGTGATGCTGTAGTCGTGATTTATATATGCTTGATTTTTGCTTCCT 60	Qy 61 TCTTTATACTTTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAAT 120	Oy 121 AAATTATCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAAGGAAAGTTAGCCCTAT 180	Ay 181 CGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTCTAAGTCCTCTGT 240	Oy 241 TITCITIGAGCAGAAAGAGAAAGCAGTCACCCTCTCTTCCATGACAACAACCATGACC 300
c 89 42 7.9 13449 13 US-10-311-455-1357 Sequence 1357, Ap 2 41.8 7.9 284 13 US-09-814-353-7553 Sequence 33, Appl 92 41.8 7.9 396 9 US-09-825-294-33 Sequence 33, Appl 93 41.8 7.9 396 10 US-09-970-966-33 Sequence 33, Appl 94 41.8 7.9 396 12 US-10-369-186-33 Sequence 33, Appl 95 41.8 7.9 396 12 US-10-369-186-33 Sequence 33, Appl 96 41.8 7.9 396 14 US-10-212-677-33 Sequence 33, Appl 96 41.8 7.9 513509 11 US-09-754-853A-4 Sequence 1004, Ap 841.6 7.9 298 10 US-09-814-353-17818 Sequence 1004, Ap 841.6 7.9 384 13 US-09-814-353-17818 Sequence 18604, Ap 100 41.6 7.9 384 13 US-09-814-353-18604 Sequence 5368, Appl 100 41.6 7.9 385 13 US-09-814-353-5368 Sequence 5368, Appl 100 41.6 7.9 385 13 US-09-814-353-5368	ALIGNMENTS	RESULT 1 US-10-027-632-1 i Sequence 1, Application US/10027632 i Publication No. US20030204075A9 i GENREAL INPORMATION: i APPLICATION WANTON David G. i TITLE OF INVENTION: Delymorphisms in the Human Genome i TITLE OF INVENTION: Polymorphisms in the Human Genome i TITLE OF INVENTION: DOWNORDER: US/10/027,632 CURRENT FILING DATE: 2002-04-30 CURRENT FILING DATE: 2000-07-12 i PRIOR PLING DATE: 2000-07-12 i PRIOR PLING DATE: 2000-04-20 i PRIOR PLING DATE: 2000-04-20 i PRIOR PLING DATE: 2000-04-20 i PRIOR PLING DATE: 2000-04-20 i PRIOR APPLICATION NUMBER: US 60/198,676 i PRIOR PLING DATE: 2000-04-20 i PRIOR APPLICATION NUMBER: US 60/198,218 PRIOR PLING DATE: 1999-11-23 i PRIOR PLING DATE: 1999-11-23 i PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR APPLICATION NUMBER: US 60/166,358 PRIOR APPLICATION NUMBER: US 60/166,358 PRIOR APPLICATION NUMBER: US 60/146,002 i PRIOR PLING DATE: 1999-09-28 i PRIOR PLING DATE: 1999-09-28 i PRIOR PLING DATE: 1999-09-28 i PRIOR PLING DATE: 1999-00-28 i PRIOR PLING DATE: 1999-00-28 i PRIOR PLING DATE: 1999-00-28 i PRIOR PLING DATE: 1999-00-28 i PRIOR PLING DATE: 1999-00-28 i PRIOR PLING DATE: 1999-00-28 i PRIOR PLING DATE: 1999-00-38 i PR	Query Match 99.9%; Score 528.6; DB 13; Length 529; Best Local Similarity 100.0%; Pred. No. 1.5e-119; Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 CATGGTGATGCTGTAGTCGTGGCTGATTTATAGTGGTGATTTTGCTTCCT 60	OY 61 TCTTTATACTTTATTATTCCCAAATTTTCTTAAGCAATATTTCTTGCTAATCAAT 120 Db 61 TCTTTATACTTTATTTATTCCCAAATTTTCTTAAGCAAATATTTCTTGCTAATCAAT 120	OY 121 AAATTATCAAAAGAAAAAAACTGAAAGGAACGCTTGAAAAAAGGAAAGTTAGCCCTAT 180 	OY 181 CGGGTATATTTGGAAGTTGTAAAATACTACRTGTTCTCTTCTAAGTCCCACTCCTCTG 240	OY 241 TITCITIGAGCAGGAAAGCAGTCACCCTCTCTTCCATGACAACACCCATGACC 300

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US-10-027-632-300106

US-10-027-632-300106

Equence 300106, Application US/10027632

EDULication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: IDENTIFY BOLD TOWNER: US/10/027,632

CURRENT APPLICATION NUMBER: US/0066

PRIOR PELICATION NUMBER: US 60/18,006

PRIOR FILING DATE: 2000-07-12

PRIOR PELICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR PELICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR PELICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR PELICATION NUMBER: US 60/167,363

PRIOR PELICATION NUMBER: US 60/167,363

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PRIOR PELICATION NUMBER: US 60/167,363

PRIOR PELICATION NUMBER: US 60/167,363

PRIOR PELICATION NUMBER: US 60/167,363

PRIOR PELICATION NUMBER: US 60/167,363

PRIOR PELING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: Fast-SEQ for Windows Version 4.0

SEQ ID NO 300106

LENGTH: SASE
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100.0%; Pred. No. 2.6e-119;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 528; Conservative
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; ORGANISM: Human
US-10-027-632-300106
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Sequence 54345, Application US/10027632

Sequence 54345, Application US/10027632

GENERAL INFORMATION:
INTER OF INVENTION: David G.
ITLE OF INVENTION: David G.
ITLE OF INVENTION: David G.
ITLE OF INVENTION: David G.
ITLE OF INVENTION: David G.
ITLE OF INVENTION: David G.
ITLE OF INVENTION: DAVID CO.04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-07-12

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-89

PRIOR PILING DATE: 1999-09-89

PRIOR PILING DATE: 1999-09-89

PRIOR PILING DATE: 1999-08-09

PRIOR PILING DATE: 1999-08-09

PRIOR PILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SEQ ID NO 54345

PRIOR PILING DATE: 1999-08-09

LENGTH APPLICATION NUMBER: US 60/146,002

PRIOR PILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SEQ ID NO 54345

PRIOR PILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

PRIOR PILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720
                                                   421 AGCTGTTCGGGGACTTCCAGAATAAACCAAACCAGCTGTATTACTGGTCTTTGACATCCT
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Best Local Similarity 100.
Matches 528; Conservative
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US-10-027-632-54345
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITILE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PLING DATE: 2002-04-30
FRIOR PELING DATE: 2000-07-12
FRIOR PELING DATE: 2000-07-12
FRIOR PELING DATE: 2000-04-20
FRIOR PELING DATE: 2000-04-20
FRIOR PELING DATE: 2000-04-20
FRIOR PELING DATE: 2000-03-24
FRIOR PELING DATE: 1999-11-23
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FRIOR PELING DATE: 1999-11-23
FRIOR PELING DATE: 1999-10-09-09
FRIOR FILING DATE: 1999-08-09
FRIOR PELING DATE: 1999-08-09
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100.0%; Pred. No. 2.6e-119;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 300106, Application US/10027632; GENERAL INFORMATION:
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Matches 528; Conservative
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| Sequence 54345, Application US/10027632
| GENERAL INFORMATION:
| TATLE OF INVENTION: Identification and Mapping of Single Nucleotide
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: Polymorphisms in the Human Genome
| TITLE OF INVENTION: 1080-1.129
| TITLE OF INVENTION: POLYMORE 10810/027,632
| CURRENT APPLICATION NUMBER: US/10/027,632
| CURRENT FILING DATE: 2000-07-12
| PRIOR PELLING DATE: 2000-07-12
| PRIOR APPLICATION NUMBER: US 60/193,483
| PRIOR APPLICATION NUMBER: US 60/193,483
| PRIOR PELLING DATE: 2000-03-29
| PRIOR PELLING DATE: 2000-03-29
| PRIOR PELLING DATE: 1999-11-23
| PRIOR APPLICATION NUMBER: US 60/167,363
| PRIOR APPLICATION NUMBER: US 60/166,358
| PRIOR PELLING DATE: 1999-01-123
| PRIOR PELLING DATE: 1999-09-18-23
| PRIOR PELLING DATE: 1999-09-18-23
| PRIOR PELLING DATE: 1999-09-09
| NUMBER OF SEQ ID NOS: 325270
| SOFTWARE FRANCE FRANCE FRANCE FRANCE FROM WINDOWS VETBION 4.0
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100.0%; Pred. No. 2.6e-119;
iive 0; Mismatches 0;
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Best Local Similarity
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US-10-027-632-54345
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US-10-027-632-54345
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APPLICANT: Lee, John
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-25
PRIOR PELING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-07
PRIOR PLING DATE: 2000-07-25
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PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-07-25
PRIOR PLING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SEC ID NO 178-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 17876, Application US/09814353
; Publication No. US20030165831A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANAAAAAAAAAAAAAAAAAA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: misc_feature
; LOCATION: 206, 227
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-17876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-814-353-17876
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APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nongbing
APPLICANT: Byat., John C.
TITLE OF INVENTION: WUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: WUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: WUSCEL AND FAT DEPOSITION
TITLE OF INVENTION: WUSCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
LENGTH: 424
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APPLICANT: Libilite, Jamela

APPLICANT: Thompson, Pamela

APPLICANT: Libilite, Jamela

APPLICANT: Libilite, Jamela

APPLICANT: Libilite, Jamela

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND

FILE REFERENCE: MRI-OGG 13-21

CURRENT APPLICATION NUMBER: US 60/191,031

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-06-15

PRIOR PAPLICATION NUMBER: US 60/216,920

PRIOR FILING DATE: 2000-06-15

PRIOR PLICATION NUMBER: US 60/216,920

PRIOR FILING DATE: 2000-07-07

PRIOR PLICATION NUMBER: US 60/220,661

PRIOR FILING DATE: 2000-07-20

PRIOR PLICATION NUMBER: US 60/257,672

PRIOR PLICATION NUMBER: US 60/257,672

PRIOR PLICATION NUMBER: US 60/257,672

PRIOR PLICATION NUMBER: US 60/257,672

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PRIOR PLICATION NUMBER: US 60/257,672
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ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 48-LIB3058-026-Q1-K1-D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.6%; Score 51; DB 13; Best Local Similarity 61.8%; Pred. No. 0.013; Matches 81; Conservative 0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-960-352-11218/c
. Sequence 11218, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
Sequence 17553, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
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US-09-814-353-17553
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TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determi
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
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APPLICANT: Thompson, Pamela
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, Jamela
APPLICANT: Lillie, Jamela
APPLICANT: Lillie, Jamela
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILE REPERRICE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT APPLICATION NUMBER: US 60/191,031
PRIOR PILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
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PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 98, 119, 145, 154, 170, 172, 193, 207, 212, 213, 214,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .... 9.0%; Score 47.4; DB 13; Length 113515; l. Similarity 54.4%; Pred. No. 2; 93; Conservative 1; Mismarchon --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-2148
                                                                                                     FILE TREATMENT APPLICATION NUMBER: US/10/311,455
CURRENT PILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2000-09-01
NUMBER: OF SEQ 1D NOS: 2424
LENGTH: 113515
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4872
LENGTH: 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4872, Application US/09814353; Publication No. US20030165831A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 93; Conserv
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US-09-814-35-16036/c
; Sequence 16036, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Lilie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; TITLE OF INVENTION: UDBNIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: UDBNIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: UDBNIFICATION, UDBER: US 60/191,031
; FRIOR APPLICATION NUMBER: US 60/201,124
; PRIOR FILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SEOFTAME: PRACESED FOR WINDOWS VETSION 4.0
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                                                           Length 424;
                                                                                                                 Indels
                                                        9.4%; Score 49.6; DB 10;
59.0%; Pred. No. 0.034;
tive 0; Mismatches 59;
                                                                                                                                                                          26 ATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                        146 AAAGCAACGCTTGAAAAAAGGAAA 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.2%
The 74; Conservative
                                                        Query Match
Best Local Similarity 59.0
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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US-09-960-352-11218
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Sequence 8414, Application US/09960352

Patent No. US20020137139A1

GENERAL INFORMATION:
   APPLICANT: Wasley C.
   APPLICANT: Tao, Nengbing
   APPLICANT: Byatt, John C.
   APPLICANT: Mathialagan, Nagapan
   APPLICANT: Byatt, John C.
   APPLICANT: Mathialagan, Nagapan
   APPLICANT: Mathialagan, Nagapan
   TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
   FILE REFERENCE: 16511.006/37-21(10298) C
   CURRENT APPLICATION NUMBER: US/09/960,352
   CURRENT PLING DATE: 2001-09-24
   NUMBER OF SEQ ID NOS: 15112
   SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                          81 CCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAA 140
                                                                                                                                                                                                                                                                                                                          27 TITATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATATTCCCAAA 86
                                                                                                                                                                                                                                                                   Sequence 18006, Application US/09814353
Publication No. US20030165831A1
GERERAL INFORMATION:
APPLICANT: Lie, John
APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
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                                                                                             Length 597;
                                                                                                                                                52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Bos taurus
CTHER INFORMATION: Clone ID: 36-LIB3058-048-Q1-K1-A8
US-09-960-352-8414
                                                                                       Score 47.2; DB 13;
Pred. No. 0.16;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 AACTGAAAGCAACGCTTGAAAAAAGGAAA 169
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         OTHER INFORMATION: n = A, T, C or
                                                                                       Query Match
Best Local Similarity 59.4%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 57.0
Matches 85; Conservative
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                  ; OTHEK INFORMALL
US-09-814-353-11169
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Sequence 11169, Application US/09814353

Publication No. US20030165831A1

GENERAL INFORMATION:

APPLICANT: Lee, John

APPLICANT: Thompson, Pamela

APPLICANT: Thompson, Pamela

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: THERRAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERRAPY OF OVARIAN CANCER

FILE REFERENCE: MIL 1006

CURRENT APPLICATION NUMBER: US 60/191,031

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-25

PRIOR PILING DATE: 2000-06-25

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-06-15

PRIOR PILING DATE: 2000-07-07

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                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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NAME/KEY: misc feature
LOCATION: 1, 98, 119, 145, 154, 170, 172, 193, 207, 212, 213, 214,
LOCATION: 216, 219, 225, 236, 241, 242, 244, 258, 267, 275, 278, 293,
LOCATION: 298, 307, 310, 311, 312, 313, 316, 323, 340, 343, 350, 351,
LOCATION: 369, 384, 385, 386, 396, 404, 405, 409, 417, 419, 420
PERTURE INFORMATION: n = A,T,C or G
PERTURE:
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LOCATION: 216, 219, 225, 236, 241, 242, 244, 258, 267, 275, 278, 293, LOCATION: 298, 307, 310, 311, 312, 313, 316, 323, 340, 343, 350, 351, LOCATION: 369, 384, 385, 386, 396, 404, 405, 409, 417, 419, 420 OTHER INFORMATION: n = A,T,C or G FRATURE:
NAME/KEY: misc_feature
LOCATION: 421, 423, 440, 445, 446, 449, 453, 458, 459, 461, 477, 480, LOCATION: 421, 425, 508, 512, 516, 521, 571, 572, 573, 574, 575, 576, 577, COTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477,
576,
                                                                                                                                                                                                                                                                                                                                                     Score 47.2; DB 13; Length 597;
Pred. No. 0.16;
0; Mismatches 52; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461,
575,
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521,
589
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516,
588,
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 59.4%;
Matches 76; Conservative C
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421, 423, 440, 4
482, 508, 512, 5
578, 579, 580, 5
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 AAGNAAAG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 AAGCAACG 154
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LOCATION: 4
LOCATION: 4
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Sequence 2, Application US/10312841
CHALL CALL OF US/2030186277A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 3673778
                                                                                                                                                                                                    APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: NUSCLE AND FAT DEPOSITION
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 8414
LENGTH: 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 CTGATTTATATGCTGATTTATGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3673778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 36-LIB3058-048-Q1-K1-A8
US-09-960-352-8414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46.2; DB 10;
Pred. No. 0.2;
0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.7%; Score 46;
57.7%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8414, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1%;
Matches 84; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82; Conservative
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Best Local Similarity
Matches 82; Conserv
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; LOCATION: (379615)
US-10-312-841-2
                                                                         RESULT 17
US-09-960-352-8414/c
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; Sequence 8192, Application US/2010309479A1
; Sequence 8192, Application No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Workward.
; APPLICANT: Workward.
; APPLICANT: Woodward, Robert
; APPLICANT: Woodward, Robert
; APPLICANT: Woodward, Robert
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS POR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS POR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT PELLOR DATE: 2001-06-08
; PRIOR FILING DATE: 2001-06-08
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFFWARE: Patentin version 3.1
; SEC 1D NO 9192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 TGCTAATCAATAATTATCAAAAGAAAAAAAACTGAAAGGCAAGGCTTGAAAAAAGGAAA 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 GAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AAAAAAAAAAAAAAATAAAAAAAAAAAAAAAAAAA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.8%; Score 46.6; DB 13;
Best Local Similarity 56.1%; Pred. No. 0.18;
Matches 88; Conservative 0; Mismatches 69;
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR PLING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-15
PRIOR PELICATION NUMBER: US 60/211,940
PRIOR PELICATION NUMBER: US 60/216,820
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18006
LENCTH: 383
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Best Local Similarity 61.74
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-09-814-353-18006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-10-131-827-8192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 16
US-10-131-827-8192/c
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LENGTH: 480
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146 TITINGGGGAAAAAAAAAAAAAAAANCNNTTTTTTNNCCCCCCCCCNNATTTTT 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 TATTITIGGAAGTIGTAAAATACTACRIGTICTICTAAGTCCCACTCCTCTGTTTTCTT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127 TCAAAAGAAAAAAAAACTGAAAGCAACGCTTGAAAAAAAGGAAAGTTAGCCCTATCGGGTA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 TAAAAAAAAAAANCNTTTTTTTTTTTTTTTTAAAAAANNNNAAANNGNNNNTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAWE/KEY: misc_feature
LOCATION: 57, 58, 59, 60, 100, 102, 128, 129, 130, 131, 132, 133, 137,
LOCATION: 138, 140, 141, 142, 143, 150, 174, 176, 177, 184, 185, 190,
LOCATION: 198, 199, 208, 209, 210, 211, 212, 213, 219, 222, 232, 234,
LOCATION: 249, 252, 253, 254, 263, 264, 265, 268, 269, 276
OTHER_INFORMATION: n = A,T,C or G
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351,
408,
                                                                                                                                                                                                        302,
350,
406,
438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301,
349,
403,
437,
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346,
395,
433,
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345,
394,
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344,
389,
429,
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NAME/KEY: misc_feature
LOCATION: 439, 440, 441, 442, 444, 451
DOTHER INFORMATION: n = A,T,C or G
US-09-814-353-11146
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340,
387,
428,
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LOCATION: 284, 286, 294, 295, 296,
LOCATION: 313, 314, 325, 326, 335,
LOCATION: 359, 367, 379, 382, 386,
LOCATION: 409, 413, 414, 424, 426,
OTHER INFORMATION: n = A,T,C or G
                                                                   247 TGAGCAGGAAAGAGAAG 264
                                                                                                            206 TINNNNNNAAAANAANG 223
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67 TACTITIATITIATICCCAAATITITICTTAAGCAAATATTTCTTTGCTAATCAATAAATTA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 TAAAAAAAAAAAAINCNTTTTTTTTTTTTTTTAAAAAANNNNNAAANNGNNNNTT 145
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                                                                                                                                                                                    Sequence 4849, Application US/09814353
; Sequence 4849, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Lee, John
; APPLICANT: Lillie, Jame9
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: IDENTIFICATION, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, AND TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; TITLE OF INVENTION: UNMERR: US 60/191,031
; FRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR APPLICATION NUMBER: US 60/257,672
; RINGRAPH OF SEQ ID NOS: 22037
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: 57, 58, 59, 60, 100, 102, 128, 129, 130, 131, 132, 133, 137,
LOCATION: 138, 140, 141, 142, 143, 150, 174, 176, 177, 184, 185, 190,
LOCATION: 138, 199, 208, 209, 210, 211, 212, 213, 219, 222, 232, 234,
LOCATION: 249, 252, 253, 254, 263, 264, 265, 268, 269, 276
OTHER INFORMATION: n = A,T,C or G
FEATURE:
LOCATION: 284, 286, 294, 295, 296, 297, 298, 299, 300, 301, 302, 311,
LOCATION: 359, 367, 379, 385, 386, 387, 389, 394, 395, 403, 406, 408,
LOCATION: 359, 367, 379, 386, 387, 389, 394, 395, 403, 406, 408,
OTHER INFORMATION: n = A,T,C or G
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8.7%; Score 45.8; DB 13; Length 463;
Best Local Similarity 44.9%; Pred. No. 0.3;
Matches 89; Conservative 1; Mismatches 108; Indels 0.
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| NAME/KEY: misc_feature
| LOCATION: 439, 440, 441, 442, 444, 447, 451
| COCATION: 0 = A,T,C or G
| US-09-814-353-4849
                                                                                                   88140 AACAAATAAACACGTAAACAAA 88119
                                                                 CTGAAAGCAACGCTTGAAAAA 164
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPERRACE: MRI-0068
CURRENT APPLICATION NUMBER: US/09/814,353
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.6%; Score 45.6; DB 13; Length 406; Best Local Similarity 56.2%; Pred. No. 0.32; Matches 81; Conservative 0; Mismatches 63; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 359
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8.5%; Score 45; DB 13; Length 35
Best Local Similarity 53.0%; Pred. No. 0.42;
Matches 96; Conservative 0; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 ATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-15
PRIOR PELICATION NUMBER: US 60/211,940
PRIOR PELICATION NUMBER: US 60/211,940
PRIOR PELICATION NUMBER: US 60/216,820
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17359
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 17782
LENGTH: 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 AAAAAAAAAAAAAAAAAAAAAAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17359, Application US/09814353
Publication No. US20030165831A1
                                                                                                                                                                                                                                                            FEATURE:
| NAME/KEY: misc feature
| LOCATION: 225, 226, 227, 228
| OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
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TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHG
FILE REFERENCE: BOL/1208/WO
CURRENT PELLOR TION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITITAILITALICCCAAAITITICITAAGCAAAIAITITCITIGCIAAICAAIAAATIAIC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 TTTTGGAAGTTGTAAAATACTACRTGTTCTCTAAGTCCCACTCCTCTGTTTTCTTTG 248
     RESULT 22
US-09-814-353-17782/C
; Sequence 17782, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Lee, John
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; TILLE OF INVENTION: USBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR PILING DATE: 2000-03-21
; PRIOR FILING DATE: 2000-05-25
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-07-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/10312841; Publication No. US20030186277A1; GENERAL INFORMATION:
                                                                                    247 TGAGCAGGAAAGAGAAG 264
                                                                                                                                     206 TINNNNNNAAAAANAANG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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Matches 104; Conserv
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LOCATION: (3294164)
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                                                                                                                                        149 rirrinaarirrrrrririrrirrigaararararirrirrrrarrrraaaaarararr 208
                                                                                                                                                                                                               132 AGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTT 191
                                                                                                                                                                                                                                                                                 209 TTTAAAATAAAAAAAAGGGAAAAAAAAAAAAAAAAATTTAGTTTATTCTTGTAGGGTT 268
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8.5%; Score 44.8; DB 13;
Best Local Similarity 61.4%; Pred. No. 0.44;
Matches 70; Conservative 0; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:

NAME/KEY: mlsc_feature

LOCATION: 206, 227

OTHER INFORMATION: n = A,T,C or G
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US-09-814-353-17876/c
                                                                                                                                                                                                                                                                                                                                                       192 T 192
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Sequence 4726, Application US/09814353 Publication No. US20030165831A1 GENERAL INFORMATION: APPLICANT: Lee, John APPLICANT: Thompson, Pamela

RESULT 25 US-09-814-353-4726/c

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49 ATTTTGCTTCCTTCTTTATACTTTTATTTTCCCAAATTTTTTCTTAAGCAAATATTTCT 108
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| NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: misc_feature | NAME/KEY: 
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, ADDITITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF OVARIAN CANCER FILE REFERENCE: MRI-006B

CURRENT FILING DATE: 2001-03-21

PRIOR PILING DATE: 2001-03-21

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-05-25

PRIOR PLING DATE: 2000-06-15

PRIOR PLING DATE: 2000-06-15

PRIOR PLING DATE: 2000-06-15

PRIOR PLING DATE: 2000-07-07

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PRIOR PLING DATE: 2000-07-25
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714
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Eublication No. US70030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
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8.5%; Score 44.8; DB 13;
Best Local Similarity 57.9%; Pred. No. 0.67;
Matches 70; Conservative 0; Mismatches 51;
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NAME/KEY: misc_feature

LOCATION: 686, 689, 699, 692, 694, LOCATION: 701, 703, 704, 706, 711, 713, 0THER INFORMATION: n = A,T,C or G
US-09-814-353-4726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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Query Match
Best Local Similarity 59.5'
Matches 75; Conservative
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ORGANISM: Homo sapiens
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US-09-834-975-451
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713, 714
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Publication No. US20030165831A1

GENERAL INFORMATION:
APPLICANT: Lee, John Pamela
APPLICANT: Lilie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE REPRESENCE: MRI-0068
FILE REPRESENCE: MRI-0068
CURRENT APPLICATION NUMBER: US/09/814,353
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8.5%; Score 44.8; DB 13; Length 723;
Best Local Similarity 57.9%; Pred. No. 0.67;
Matches 70; Conservative 0; Mismatches 51; Indels 0
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518,
586,
653,
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515,
581,
645,
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491,
578,
643,
THERAPY OF OVARIAN CANCER
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483,
561,
639,
            THILE OF INVENTION: THERAFT OF CONTRIAN CANDER CURRENT APPLICATION NUMBER: US/09/814,353 CURRENT FILING DATE: 2001-03-21 PRIOR FILING DATE: 2000-03-21 PRIOR PELICATION NUMBER: US 60/191,031 PRIOR FILING DATE: 2000-05-25 PRIOR PELICATION NUMBER: US 60/201,24 PRIOR PILING DATE: 2000-05-25 PRIOR PILING DATE: 2000-05-25 PRIOR PELICATION NUMBER: US 60/216,820 PRIOR PILING DATE: 2000-07-7 PRIOR PELICATION NUMBER: US 60/226,661 PRIOR PELICATION NUMBER: US 60/257,672 PRIOR PELICATION NUMBER: US 60/257,672 PRIOR APPLICATION NUMBER: US 60/257,672 PRIOR PILING DATE: 2000-07-25 PRIOR PILING DATE: 2000-07-25 PRIOR PILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 22037 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11024
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482,
558,
627,
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NAME/KEY: misc_feature
LOCATION: 686, 689, 689, 690, 692,
LOCATION: 701, 703, 704, 706, 711,
OTHER INFORMATION: n = A,T,C or G
US-09-814-353-11024
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  OF INVENTION:
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Sequence 451, Application US/09834975

Sequence 451, Application US/09834975

Patent No. US20020110815A1

SERNEMAL INFORMATION:

APPLICANT: Iniliae, James

APPLICANT: Brown, Jeffrey

APPLICANT: BOLK, Andrew

APPLICANT: BOLK, Andrew

TITLE OF INVENTION: OP HUMAN CANCERS

TITLE OF INVENTION: OP HUMAN CANCERS

TITLE OF INVENTION: OP HUMAN CANCERS

TITLE OF INVENTION: OP HUMAN CANCERS

TITLE OF INVENTION: OP HUMAN CANCERS

TITLE OF INVENTION: OP HUMAN CANCERS

TITLE OF INVENTION: OP HUMAN CANCERS

FILE REFERENCE: MRI-016B

CURRENT APPLICATION NUMBER: US/09/834,975

CURRENT APPLICATION NUMBER: 60/197,538

PRIOR FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 1046

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 451

LENGTH: 4.25
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59.5%; Pred. No. 0.47;
tive 0; Mismatches 51;
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8.4%; Score 44.4; DB 10;
Best Local Similarity 54.9%; Pred. No. 0.64;
Matches 84; Conservative 0; Mismatches 69;
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-07-25
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: Feastseq for Windows Version 4.0
SEQ ID NO 17588
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NAME/KEY: misc_feature
LOCATION: (1)...(425)
OTHER INFORMATION: n = A,T,C or G
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Sequence 66, Application US/10055098

Publication No. US200301399541

GENERAL INFORMATION:

APPLICANT: ROBEN et al.

TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ032P1

CURRENT APPLICATION NUMBER: US/10/055,098

CURRENT FILING DATE: BARLIER PILING DATE: 1000-02-23

PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-24

PRIOR FILING DATE: EARLIER PILING DATE: 1999-08-24

PRIOR FILING DATE: EARLIER PILING DATE: 1999-08-24

PRIOR PLING DATE: EARLIER PILING DATE: 1999-08-25

PRIOR PLING DATE: EARLIER PILING DATE: 1999-08-25

PRIOR PLING DATE: EARLIER PILING DATE: 1999-08-25

PRIOR PLING DATE: EARLIER PILING DATE: 1999-08-25

PRIOR PLING DATE: EARLIER PILING DATE: 1999-08-25

PRIOR FILING DATE: EARLIER PILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 66

LENGTH: 664
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Pred. No. 0.8;
1; Mismatches 82;
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NAME/KEY: SITE
LOCATION: (31)
OTHER INFORMATION: n equals a,t,g, or c, nAME/KEY: SITE
LOCATION: (63)
OTHER INFORMATION: (63)
OTHER INFORMATION: n equals a,t,g, or c
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; OTHER INFORMATION: n equals a,t,g, or c
US-10-055-098-66
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              PRIOR APPLICATION NUMBER: 60/097,917
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/098,634
PRIOR PILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 52.8%;
Matches 93; Conservative
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                               8.41
Best Local Similarity 52.81
Matches 93; Conservative
                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-055-098-66/c
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147 AAGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        521 AAAAACCTCACAATAAATTAAATTTTTACACTATGAAGTACACATTGGAATTTGAA 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
8.4%; Score 44.4; DB 9;
Best Local Similarity 52.8%; Pred. No. 0.8;
Matches 93; Conservative 1; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                            GENERAL INTEGRATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ032P1
CURRENT APPLICATION NUMBER: US/09/739,254
CURRENT FILING DATE: 2000-12-19
EARLIER APPLICATION NUMBER: 09/511,554
EARLIER APPLICATION NUMBER: 09/511,554
EARLIER APPLICATION NUMBER: 09/511,554
EARLIER APPLICATION NUMBER: 00/097,917
EARLIER FILING DATE: 1999-08-24
EARLIER FILING DATE: 1999-08-24
EARLIER FILING DATE: 1999-08-25
EARLIER FILING DATE: 1998-08-15
EARLIER FILING DATE: 1998-08-15
SARLIER FILING DATE: 1998-08-16
SARLIER FILING DATE: 1998-08-16

LENGTH: 664
                                                                                                                                147 AAGCAACGCTTGAAAAAGGAAAGTTAGCCCTA 179
                                                                                                                                                                           131 AAAAAAAAAAAAAAAAAAAAAAATTTCCCCCA 163
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Fatent No. US20020026040A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERRINCE: PZ03ZP1
CURRENT FALING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 08/09/904,615
PRIOR APPLICATION NUMBER: 09/511,554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) LOCATION: (63)
; OTHER INFORMATION: n equals a,t,g,
US-09-739-254-66
                                                                                                                                                                                                                                                                                      Sequence 66, Application US/09739254
Patent No. US20010021700A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (31)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
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US-09-904-615-66/c
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Sequence 1, Application US/10312841
| Publication No. US20030186277A1
| Publication No. US20030186277A1
| APPLICANT: Epigenomics AG | TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC | TITLE OF INVENTION: USA08/WO | CURRENT APPLICATION NUMBER: US/10/312,841
| CURRENT RILING DATE: 2002-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      886838 TGGTTTTTGTGTTTTGTGTTTTTATCGTTATTTTTTAAGTTTTTTTAGTATATTTGATA 686897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 TATACTTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAAT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 TATCAAAAGAAAAAAAAACTGAAAGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 TATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 6078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.4%; Score 44.4; DB 13;
Best Local Similarity 54.4%; Pred. No. 2.5;
Matches 87; Conservative 1; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 TATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13;
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              FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
FRIOR APPLICATION NUMBER: PCT/EP01/07537
FRIOR FILING DATE: 2001-07-02
FRIOR APPLICATION NUMBER: DE 10032529.7
FRIOR FILING DATE: 2000-06-30
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR FILING DATE: 2000-09-01
NUMBER: OF SEQ ID NOS: 2424
SEQ ID NO 1110
LENGTH: 6078
cytosine methylation
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Best Local Similarity
Matches 100; Conserv
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; LOCATION: (3294164)
US-10-312-841-1
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US-10-111-455-1110/c
US-10-1110, Application US/10311455
; Publication No. US2003014506A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BIRLIN, Kurt
; APPLICANT: BIRLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
                                                                                                              TTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAAACTGA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITATATACCEGATITATGGGTGATITTGCTTCCTTTATACTTTTATTTCCCAAA 86
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Pred. No. 0.8;
1; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILLE REFERENCE: P2012P1
CURRENT APPLICATION NUMBER: US/10/054,988
CURRENT FILING DATE: 2002-01-25
PRIOR PLICATION NUMBER: 09/904,615
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
PRIOR FILING DATE: 1998-08-25
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COTHER INFORMATION: n equals a,t,g, or US-10-054-988-66
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Publication No. US20030087341A1
GENERAL INFORMATION:
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Best Local Similarity 52.8%;
Matches 93; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (31)
OTHER INFORMATION:
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                                                                                                            87
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us-10-027-632-1.rnpb

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PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8434
                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: 1
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APPLICANT: Lee, John
APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPERBNCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILLING DATE: 2000-03-21
PRIOR PELICATION NUMBER: US 60/191,031
PRIOR FILLING DATE: 2000-05-25
PRIOR PELICATION NUMBER: US 60/207,124
PRIOR PLING DATE: 2000-05-25
PRIOR PELING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PILING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR PELING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR PELING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR APPLICATION NUMBER: US 60/257,672
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-25
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PRIOR PELING DATE: 2000-07-25
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Pred. No. 0.65;
0; Mismatches 60; Indels
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Publication No. US2003009974A1
GENERAL INFORMATION:
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
TILLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
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CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
                                                                                                                                                                                                                            Sequence 17383, Application US/09814353
Publication No. US20030165831A1
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                                                                              687018 ATTTTAAAATATT 687030
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Best Local Similarity 57.1%;
Matches 80; Conservative
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US-09-814-353-17383
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ID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 GAAAAAAAAACGAAGGAAGGTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.3%; Score 43.8; DB 10; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                     533,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.3%; Score 44; DB 15; Length 60 Best Local Similarity 48.7%; Pred. No. 0.96; Matches 95; Conservative 0; Mismatches 100; Indels
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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 52-LIB3058-016-Q1-K1-E12
US-09-960-352-12183
                                                                                                                                                                                                                                                                                                                                                                                     527,
563,
599
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
TILLE OF INVENTION: NUCLBIC ACID AND OTHER MOLECUI
TILLE OF INVENTION: MUSCLE AND PAT DEPOSITION
FILE REPERRINCE: 16511.006/37-21(10298) C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILLING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 12183
                                                                                                                                                                                                                                                                                                                                                                                     526,
562,
598,
NAME/KEY: misc_feature
LOCATION: 2, 14, 27, 61, 150, 153, 156,
LOCATION: 229, 230, 234, 236, 288,
LOCATION: 323, 324, 325, 326, 330,
LOCATION: 346, 349, 350, 351, 352, 368,
OTHER INFORMATION: n = A,T,C or G
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561,
594,
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                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; LOCATION: 518, 519, 520, 521, 522,
; LOCATION: 536, 537, 538, 541, 559,
; LOCATION: 570, 575, 589, 590, 592,
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-8434
                                                                                                                                                                                                    LOCATION: 374, 375, 376, 377, 379, LOCATION: 401, 402, 403, 404, 406, LOCATION: 477, 435, 436, 437, 444, LOCATION: 478, 479, 480, 481, 483, OTHER INFORMATION: n = A,T,C or G
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FEATURE:
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                                        Gaps
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ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
ITILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
ITILE OF INVENTION: THERAPY OF OVARIAN CANCER
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
FRIOR APPLICATION NUMBER: US 60/191,031
FRIOR APPLICATION NUMBER: US 60/211,24
FRIOR APPLICATION NUMBER: US 60/211,940
FRIOR FILING DATE: 2000-05-25
FRIOR FILING DATE: 2000-05-25
FRIOR FILING DATE: 2000-07-25
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0.67;
-rhes 62; Indels
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56.6%; Pred. No. 0.73;
                                     0; Mismatches
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         Pred. No.
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Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
                                                                                                                                                                                                                                                                                                                                      147 AAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                             167 AATGTTAĞTGİĞAAAATGACAAA 189
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      56.68;
      Best Local Similarity 56.6
Matches 81; Conservative
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ORGANISM: Homo sapiens
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US-09-814-353-17383/c
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US-09-814-353-5380
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Sequence 5380, Application US/09814353; Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John

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, 308, 322, 330, 335,
, 367, 371, 377, 384,
, 454, 455, 456
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550, 554, 568,
      APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPRENCE: MRI-006B
CURRENT APPLICATION NUMBER: US 60/191,031
FRIOR APPLICATION NUMBER: US 60/191,031
FRIOR APPLICATION NUMBER: US 60/207,124
FRIOR PELING DATE: 2000-03-21
FRIOR PELING DATE: 2000-06-25
FRIOR APPLICATION NUMBER: US 60/211,940
FRIOR PILING DATE: 2000-06-15
FRIOR APPLICATION NUMBER: US 60/216,820
FRIOR APPLICATION NUMBER: US 60/226,661
FRIOR APPLICATION NUMBER: US 60/226,661
FRIOR APPLICATION NUMBER: US 60/257,672
FRIOR APPLICATION NUMBER: US 60/257,672
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1; Mismatches 205; Indels
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549,
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LOCATION: 224, 225, 238, 245, 248, 255, 257, 258,

LOCATION: 277, 278, 279, 280, 289, 292, 293, 302,

LOCATION: 343, 346, 348, 349, 350, 353, 365, 366,

LOCATION: 385, 398, 408, 422, 423, 440, 452, 453,

OTHER INFORMATION: n = A,T,C or G
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Pred. No. 1.1;
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547,
609
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543, 544, 9
591, 595, 6
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LOCATION: 457, 458, 459, 461, 473,

LOCATION: 497, 512, 521, 527, 540,

LOCATION: 569, 584, 586, 587, 589,

COTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 36.8%;
Matches 120; Conservative
Pamela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature LOCATION: 50, 99, 103,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
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214 AAAAAAANGNNNTTTCCCCCCCCCCNTTTTNAANCCCCCCNTNNANNAAAAAAANTTT 273
                                                                                                                                                              274 TINNNNNCCITITITGNGGNNAAAAAAAAAAAAGGGGNTTITITITITTTGCNTTTTTCCNGGA 333
                                                                                                                   267 GTCACCCTCTCCTTCCATGACAACCCATGACCGGCTGCTTGCCTGCTCCATCACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 ITAIGGGIGALTITIGCTICCTICITIAIACTITIAITIALICCCAAAITITITICTIAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Epigenomics AG
TITLE OF INVENTION: Method and nucleic acids for the differentiation
TITLE OF INVENTION: of prostate tumors
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
SOGANISM: Artificial Sequence
FEATURE:
CTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-172-086-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.3%; Score 43.8; DB 15; Length 9884; Best Local Similarity 62.2%; Pred. No. 4.4; Matches 69; Conservative 0; Mismatches 42; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/172,086
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 5
LENGTH: 9884
                                                                                                                                                                                                                                                       334 CNCCCCCCCNAANANNTTNCCCCCC 359
                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/10172086 Publication No. US20030113750A1 GENERAL INFORMATION:
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US-10-311-455-1449/c
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APPLICANT: Thompson, Pamela
APPLICANT: Lillie, James
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REPERENCE: MRI-006B
CURRENT FILING DATE: 2001-03-21
PRIOR PELICATION NUMBER: US 60/191,031
PRIOR PELICATION NUMBER: US 60/207,124
PRIOR PELICATION NUMBER: US 60/207,124
PRIOR PELICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR PELICATION NUMBER: US 60/216,820
PRIOR PELICATION NUMBER: US 60/220,661
PRIOR PELICATION NUMBER: US 60/220,661
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PASTESE for Windows Version 4.0
SOFTWARE: PASTESE FOR FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: 457, 458, 459, 461, 473, 474, 475, 476, 478, 480, 487, 494,
LOCATION: 457, 458, 521, 527, 540, 543, 544, 547, 549, 550, 554, 568,
LOCATION: 569, 584, 586, 587, 589, 591, 595, 609
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEX: misc_feature
LOCATION: 50, 99, 103, 104, 105, 106, 107, 108, 112, 114, 120, 121,
LOCATION: 122, 127, 128, 131, 132, 133, 134, 150, 151, 152, 153, 154,
LOCATION: 155, 156, 157, 158, 159, 160, 161, 162, 163, 183, 184, 186,
LOCATION: 188, 189, 190, 192, 193, 195, 196, 197, 209, 221, 223
OTHER INFORMATION: n = A,T,C or G
NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257,
293,
365,
452,
334 CNCCCCCCNAANANNTTNCCCCCC 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 224, 225, 238, 245, 248, 255,
LOCATION: 277, 278, 279, 280, 289, 292,
LOCATION: 343, 346, 348, 349, 350, 353,
LOCATION: 385, 398, 408, 422, 423, 440,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                 Sequence 11667, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
APPLICANT: Thompson, Pamela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-814-353-11667
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109 İTİTİTİTİTATITATAATAATATİTİÇAATTTAAAAATATAATTGITTAAAAATTTT 168
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APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS ITILE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
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                                                                                                                                                                                                                  Length 380;
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                                                                                                                                                                                                                                                      Indels
                                                                                                                     TYPE: DNA
ORGANISM: Bos taurus
ORGANISM: BOS taurus
US-09-960-352-9335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73;
                                                                                                                                                                                                                8.2%; Score 43.2; DB 10;
56.2%; Pred. No. 1.2;
tive 0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
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8.2%; Score 43.2; DB
Best Local Similarity 54.4%; Pred. No. 1.2;
Matches 87; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT PERFECTION NUMBER: US/09/814,353
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-05-25
PRIOR PLING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-07-07
PRIOR PILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 22037
SOFTWARE: PSELES PASSEQ for Windows Version 4.0
SSOFTWARE: PSELES
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF EQ ID NOS: 15112
LENGTH: 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 AAGCAACGCTTGAAAAAAGGAAAG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 AAAAAAATTAAAAAAAAAAAA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17565, Application US/09814353
Publication No. US20030165831A1
GENERAL INFORMATION:
APPLICANT: Lee, John
                                                                                                                                                                                                                                                        81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-814-353-17565
                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 45
US-09-814-353-17565/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Warren, Wesley C.
APPLICANT: Warren, Wengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9335, Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
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                                                                                                                                                           TTATACTTTTATTTTATTCCCAAATTTTTCTTAAGCAAATATTTTCTTTGCTAATCAATAAA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
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                                           Length 6590;
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Pred. No. 1.1;
1; Mismatches 112; Indels 0
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 GTATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTAAG 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 48-LIB3058-026-Q1-K1-D12
                                             DB 13;
                                                                               0; Mismatches
                                             Score 43.6;
Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 11218, Application US/09960352; Patent No. US20020137139A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          AAGCAACGCTTGAAAAA 164
                                                                                                                                                                                                                                                                                                              968 AATAAACACGTAAACAAA 951
                                           8.2%;
ilarity 57.2%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.2%;
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Best Local Similarity 49.3
Matches 110; Conservative
                                                             Local Similarity
tes 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-960-352-11218
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       JS-10-311-455-1449
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                                           Query Match
Best Local S
Matches 79
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
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selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient;
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                             determining whether prostate cancer has metastasized in a patient, assessing the aggressiveness or indolence of prostate cancer in a
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                                                                       (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
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(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient (f) assessing the prostate call carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
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(1) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
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(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
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                                                                                                           82 CCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAAAGAAAAAAA 141
                                                                                                                                     9
                                                           81
                                                                                                                                                                                                                                                                                                                                                     human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                   Gaps
                                 ö
     Score 50.4; DB 23; Length 556;
Pred. No. 0.02;
                                61; Indels
                                                                                                                                                                                                                                                                                                                                    Human prostate expression marker cDNA 43592.
                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 8681-8682; 11750pp; English.
                                                                                                                                                                142 ACTGAAAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                        Monahan JE;
                                                                                                                                                                                                                                                         ВР
        9.5%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-207454P.
2000US-211314P.
2000US-219007P.
                                                                                                                                                                                                                                                         ABV43601 standard; cDNA; 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-PEB-2000; 2000US-183319P.
16-MAR-2000; 2000US-189862P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2001; 2001WO-US05171
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13-DEC-2000; 2000US-255281P
                                                                                                                                                                                                                                                                                                           (first entry)
Query Match
Best Local Similarity 58.8'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                            WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                           16-SEP-2002
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from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleocide cacid molecule comprising any of 15112 nucleocide cacid comprising any of 15112 nucleocide cacid comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyademylated ribonucleotides to a 3' end cranscription and addition of polyademylated ribonucleotides to a 3' end cranscription and addition of polyademylated ribonucleotides to a 3' end complement or fragment (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid molecule or pattern of the molecule or detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid is predictive of the level or pattern of the LMFD nucleic acid is predictive of the level or pattern of the LMFD nucleic acid is used for determining a level or pattern or and the complementary nucleic acid is used for determining a level or pattern or and the complementary nucleic acid is used for determining a level or pattern or and the complementary nucleic acid is used for determining a level or pattern or and the complementary nucleic acid is used for determining a level or pattern or and the complementary nucleic acid is used for determining a level or pattern or and the complementary nucleic acid is used for determining a level or pattern or and the complementary nucleic acid is used for determining a level or pattern or and the complementary nucleic acid is used for determining a level or pattern or and the complementary nucleic acid is predictive or the laws or pattern or and the complementary nucleic acid is predictive or and the complementary nucleic acid is predictive or and the complementary nucleic acid is predictive or and the complementary nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 ATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= involved in extrachromosomal replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.4%; Score 49.6; DB 25; Length 59.0%; Pred. No. 0.028; ive 0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seqdata.uspto.gov/sequence.html?DocID=20020137139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 424 BP; 228 A; 7 C; 32 G; 157 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                improving cattle. The present sequence is one of JMFD EST (expressed sequence tag) nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium plasmid Ddp2 containing Rep gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGCAACGCTTGAAAAAAGGAAA 169
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2378..5041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ11710 standard; DNA; 5852
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(first entry)
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nes 85, Conservative
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30-JUL-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ11710;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
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            $$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$$
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                                                                                                                                                                                 selecting a composition for inhibiting prostate cancer in a patient, assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has merastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a sessessing the prostate cell carcinogenic potential of a compound; (f) assessing the prostate cancer has metastasized in a patient; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine EST associated with lactation/muscle/fat deposition #11218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid associated with lactation, and muscle and fat
                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.5%; Score 50.4; DB 23; Length 556; 58.8%; Pred. No. 0.02; ive 0; Mismatches 61; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 556 BP; 389 A; 1 C; 51 G; 113 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 ACTGAAAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AAAAAAAAAAAAAAAAAAAAAAAAAAAA 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :053/c
ABX46053 standard; cDNA; 424 BP.
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11-JAN-2000; 2000US-0480902.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 58.8
Les 87; Conservative
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MATHIALAGAN N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2002137139-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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89AU-0007187.

02-NOV-1989;

The invention relates to a purified nucleic acid molecule associated with

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DB 25; Length 424;

Monahan JE

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Schlegel R, Endege WO,
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                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                 patient
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                                                                                                                                                                                                                                                                                                                                     TTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAA 131
                                                                                                                                                                                                                                                                               71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene; ss.
                                                                                                                                                                                                                                                                                                 The sequence of Ddp2 has been found to contain the putative open reading frame indicated in the Features Table. The possible ORF is flanked by regions with similarity to promoter and poly adenylation signals of known Dictyostelium genes. The RNA and polypeptide product of the Rep gene have not, however, been detected. It is believed that the product is produced in low amounts to positively regulate initiation of plasmid replication. The polypeptide may also contain regions that act as negative regulators of plasmid copy (Updated on 25-MAR-2001 to correct PA field.)
                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                        Score 49.2; DB 12; Length 5852;
Pred. No. 0.076;
0; Mismatches 68; Indels 0;
                                                                        - of
                                                                                                                                                                                                                         Seguence 5852 BP; 2298 A; 651 C; 708 G; 2195 T; 0 other;
                                                                       Polypeptide facilitating extra-chromosomal replication recombinant plasmid in Dictyostelium species
                                                                                                                                                                                                                                                                                                                                                                         5647 AAAAAAAAATTTAAATTAAAAAAAAAAAAAAAA 5610
                                                                                                                                                                                                                                                                                                                                                       132 AGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostate expression marker cDNA 3801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                          Williams KL;
                                                                                                  Claim 15; Fig 1; 90pp; English
                                                                                                                                                                                                                                         9.3%;
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2000US-207454P.
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2000US-219007P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-2002 (first entry)
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 57.0°
Matches 90, Conservative
        (UYMA-) UNIV MACQUARIE
                          Chang ACM,
                                           WPI; 1991-164194/22.
P-PSDB; AAR11988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200160860-A2
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25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-DEC-2000;
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                          Slade MB,
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CC The invention relates to an isolated nucleic acid molecule (I) comprising

CC a nuclectide sequence given in Tables 1-9 (ABV00010-ABV62213) of the

CC specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer;

(c) assessing the efficacy of a test compound to inhibit prostate

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer;

(e) assessing the efficacy of a therapy for inhibiting prostate cancer

CC (d) assessing the prostate cell carcinocan.

(f) assessing the prostate cell carcinocan.

(g) determining whether normal carcinocan.

(h) assessing the prostate cell carcinocan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising
of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 AACCCCCNNCCAANNNNAAAANNAAAAAACCCNANNNNGACNGTAAAAAAAAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                  selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cervical cancer; cytostatic; pre-malignant condition; gene therapy; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 AAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207 ACTACRIGITCICTTCTAAGTCCCACTCCTCTTTTTTTTTGAGCAGGAAAGAGAAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCACCCTCTCCTTCCATGACAACAACCCATGACCGGCTGCTTGCCTGCTCCATCACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTATTCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.2%; Score 48.6; DB 23; Length 464; 43.3%; Pred. No. 0.05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 464 BP; 199 A; 74 C; 16 G; 116 T; 59 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cervical cancer marker nucleic acid 2745.
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25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
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                                                                                                                                                                                                                                                                                                                                                                  81; Conservative
                                                                     Endege WO,
                                                                                        WPI; 2001-662795/76.
                                                                                                                                                                                                                              cancer in a patient
                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; prostate
pharmacogenomic
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                                                                                                                                                                                                                                      (d) assessing
in a patient;
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                                                                     Schlegel R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient, and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                  TTTATATGCTGATTTATGGGTGATTTTGCTTCCTTTTATACTTTTATTTTATTCCCAAA 86
                                                                                                                                                                                                                                                                                                                                                                                     16
                                                                                                                                                                                                                   The invention relates to novel genes (AAH68727-AAH73383) associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                 isolated nucleic acid for diagnosing and treating cervical cancer for assessing and detecting compounds for treating the cancer -
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                                                                                                                            DB 22; Length 612;
                                                                                                                                                                                                                                                                                                                           Score 48.6; DB 22; Length
Pred. No. 0.054;
0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                       Sequence 612 BP; 380 A; 50 C; 2 G; 178 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate expression marker cDNA 56483.
                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                              Zhao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 ААААААААТАААААААААА 159
                                                                                                                                                                                                                                                                                                                                                                                                                                              147 AAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                Claim 1; Page 564; 1051pp; English
                                                                                                                              Berger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP
                                                99US-0171350.
2000US-0189315.
2000US-0203791.
                                                                                                                                                                                                                                                                                                                           ch 9.2%;
1 Similarity 58.7%;
84; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABV56492 standard; cDNA; 474
                    2000WO-US33312
                                       99US-0169681
                                                                                       21-JUL-2000; 2000US-0220114
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16-MAR-2000; 2000US-189862P
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                                                                                                                              Schlegel R, Deeds J,
                                                                                                                                                WPI; 2001-375006/39
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                    08-DEC-2000;
                                                          14-MAR-2000;
                                                                   12-MAY-2000;
                                                                             09-JUN-2000;
                                       08-DEC-1999;
                                                  21-DEC-1999;
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 14-JUN-2001
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; cytostatic; carcinogen; pharmacodyanamic marker;
marker; gene; 88.
                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 GCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAATTTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid molecule (I) common a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 474 BP; 234 A; 34 C; 107 G; 98 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.07;
                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 10898; 11750pp; English
                                                                                                                                              Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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13-DEC-2000; 2000US-255281P
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Homo sapiens
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                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a parlient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 AAATITITICITAAGCAAATATITICITITGCTAATGAATAAATTATCAAAAGAAAAAAAC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 TGAAAAATTINNTTITITIGAATTITINTITITITITITITICCCTTTTAAATTITIT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   selecting a composition for inhibiting prostate cancer in a patient, assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                           cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; ana
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 9.0%; Score 47.8; DB 23; Length 300; Local Similarity 56.2%; Pred. No. 0.068; es 82; Conservative 0; Mismatches 64; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 300 BP; 125 A; 22 C; 19 G; 101 T; 33 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune system associated gene SEQ ID NO: 2148
                                                                                        (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 TGAAAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
                                                                                                                   Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAAAGAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                      Claim 1; Page 750; 11750pp; English
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             ; 2000US-189862P.
; 2000US-207454P.
; 2000US-211314P.
; 2000US-219007P.
 2000US-183319P
                                                              13-DEC-2000; 2000US-255281P
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                                                                                                                                          WPI; 2001-662795/76.
                                   09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                      in a patient;
             16-MAR-2000;
25-MAY-2000;
 17-FEB-2000;
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                                                                                                               Schlegel
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Matches
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ABL34175/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 ATCAATAAATTATCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
pharmacogenomic marker; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 CTTCCTTCTTTATACTTTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 CCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTCTAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 24; Length 113515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 113515 BP; 35172 A; 1174 C; 22520 G; 54649 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.0%; Score 47.4; DB 24; Length 54.4%; Pred. No. 0.49; ive 1; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 2148; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate expression marker cDNA 44985
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01-SEP-2000; 2000DE-1043826
                                                                                                                              32-JUL-2001; 2001WO-EP07537
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93; Conservative
                                                                                                                                                                                                                                                                                                                                                           Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytosine methylation
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WO200200928-A2
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                                                                03-JAN-2002.
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Best Local &
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8.9%;
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                                                     09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
                          16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
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                                                                                                                                          Endege WO,
                                                                                                                                                                      WPI; 2001-662795/76.
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                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate call carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; carcinogen; pharmacodyanamic marker; gene; ss.
                                                                                                                                                                   Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 TTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTATTCCCAAA

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                           Claim 1; Page 8916; 11750pp; English.
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                                                                                                             Schlegel R, Endege WO, Monahan JE;
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             25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
2000US-189862P.
                                                      13-DEC-2000; 2000US-255281P
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pharmacogenomic
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleoride sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selecting a composition for inhibiting prostate cancer in a patient, assessing the prostate cell carcinogenic potential of a compound, determining whether prostate cancer has metastasized in a patient, assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                   for detecting presence of prostate cancer, stage of prostate cancer . Useful Claim 1; Page 8916. 1177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef
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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 309 BP; 188 A; 13 C; 11 G; 97 T; 0 other;
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Pred. No. 0.11;
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 8916; 11750pp; English.
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The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is affilicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine; ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                             isolated nucleic acid for diagnosing and treating cervical cancer for assessing and detecting compounds for treating the cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 8.9%; Score 47; DB 22; Length 612; Local Similarity 58.0%; Pred. No. 0.13; nes 83; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 612 BP; 380 A; 50 C; 2 G; 178 T; 2 other;
                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                             99US-0171350.
2000US-0189315.
                                      2000WO-US33312
                                                                                                                               2000US-0203791
2000US-0210600
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                                                                                         21-DEC-1999;
14-MAR-2000;
12-MAY-2000;
                                      08-DEC-2000;
                                                                                                                                                                         21-JUL-2000;
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                                                                          08-DEC-1999;
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14-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer in a patient;
                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    selecting a composition for inhibiting prostate cancer in a patient assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTCCCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 assessing the aggressiveness or indolence of prostate cancer in a
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0.12;
thes 60; Indels
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Pred. No. 0.12;
0; Mismatches
                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                        2000US-189862P.
2000US-207454P.
2000US-211314P.
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                  20-PEB-2001; 2001WO-US05171.
                                                      2000US-183319P
                                                                                                                                                   13-DEC-2000; 2000US-255281P
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                                                                                                                                                                                                                                Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                       WPI; 2001-662795/76.
                                                                                           25-MAY-2000;
                                                      17-FEB-2000;
                                                                          .6-MAR-2000;
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71

99US-115707P

12-JAN-1999;

WO200142467-A2

Homo sapiens

24-SEP-2001; 2001US-0960352

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The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide can especial appearing as ARX14836-ABX49947, or complements of them. Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that functions in the cell to cause termination of translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end coff the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising; (3) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid is predictive of the level or pattern of the complementary nucleic acid is predictive of the level or pattern of the complementary nucleic acid is used for detection of the molecule.

The LMFD nucleic acid is used for determining a level or pattern of the mapping, gene identification and analysis, cattle breeding, preparation of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of mapping, gene identification and analysis, cattle breeding in prepare in a improving cattle. The present sequence is one of the 15112 bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               t shown in the specification but from the USPTO web site:
                                                                                                                                                                                                                                                                        New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 312 BP; 167 A; 27 C; 28 G; 90 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seqdata.uspto.gov/sequence.html?DocID=20020137139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acids.
                                                                                                                                                                           Tao N, Warren WC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  he present sequence was not shown
obtained in electronic format from the
                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID No 8414; 245pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (expressed sequence tag)
11-JAN-2000; 2000US-0480902
                                                                                                                                                                        Mathialagan N,
                                              BYATT J C.
MATHIALAGAN N.
                                                                                                                                                                                                                          WPI; 2003-110599/10
                                                                                                                       (WARR/) WARREN W C.
                                                                                                  TAO N.
                                                                                                                                                                        Byatt JC,
                                              (BYAT/)
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80 84 Gaps ö DB 25; Length 312; 64; Indels Query Match 8.8%; Score 46.6; DB Best Local Similarity 57.0%; Pred. No. 0.13; Matches 85; Conservative 0; Mismatches 141 AACTGAAAGCAACGCTTGAAAAAGGAAA 169 8 셤 ò g ò

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145 ААААААААААСАААААААААААААА 173
                                              ABZ08201 standard; cDNA; 480
                                                                                  09-JAN-2003 (first entry)
                                                                ABZ08201;
                                     ABZ08201
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Human leukocyte derived cDNA SEQ ID NO 8192.

Bovine, 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification;

muscle deposition; fat depositiog. gene analysis; cattle breeding.

Bovine EST associated with lactation/muscle/fat deposition #8414.

20-FEB-2003

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169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a system for detecting gene expression, which comprises one or two isolated DNA molecules that detect expression of a gene, where the gene corresponds to any of 8143 oligonucleotides (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful for leukcyte expression profiling. It is particularly useful for diagnosing a disease, monitoring (rate of) progression of a disease, predicting therapeutic outcome, determining prognosis for a patient, predicting disease complications in an individual or monitoring response to treatment in an individual. The diseases include cardiac allograft rejection, kidney allograft rejection, liver allograft rejection, atherosclerosis, congestive heart failure, systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis or cytomegalovirus infection. The present sequence is that of a human leukocyte expressed CDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
                                 atherosclerosis; congestive heart failure; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                            New system for leukocyte expression profiling, diagnosing a disease, or monitoring (the rate of) progression of a disease, e.g. atherosclerosis or congestive heart failure, comprises diagnostic oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 TGCTAATCAATAAATTATCAAAAGAAAAAAACTGAAAGCAACGCTTGAAAAAAAGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phillips J;
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                Human; leukocyte; gene expression profiling; allograft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 8.8%; Score 46.4; DB 24; Length 480; Local Similarity 61.7%; Pred. No. 0.17; Nonservative 0; Mismatches 46; Indels 0;
                                                                                                                                                                                                                                                                                                                                         Altman P, Prentice J, Johnson F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 480 BP; 124 A; 34 C; 159 G; 163 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 26; Page 1829-1830; 2038pp; English.
                                                                                                                                                                                                                                                                                                                                         C, Matcuk G, A. Quertermous T,
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                                                                                                                                                                                                              22-OCT-2001; 2001WO-US47856.
                                                                                                                                                                                                                                               20-OCT-2000; 2000US-241994P.
                                                                                                                                                                                                                                                                                                       (BIOC-) BIOCARDIA INC.
                                                                                                                                                                                                                                                                                                                                         muth J, Fry K,
Woodward R, Qu
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-636525/68
                                                                                                                                         WO200257414-A2
                                                                                                                                                                                                                                                                                                                                           Wohlgemuth J,
                                                                                                        Homo sapiens
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(first entry)

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ABV40063 standard; cDNA; 556 BP.
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Best Local S
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                              ABV40063,
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                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMPD), derived from cattle, and the LMPD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide comparishing any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also infoluded are; (1) a transformed cell having a nucleic acid comprishing an LMPD nucleic acid linked to a promoter and a 3' nontranslated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule complementary nucleic acid molecule. The molecule; and (b) detecting the level or pattern of the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid as used to the molecule. The LMFD nucleic acid is used for determining a level or pattern of the molecule in a bovine cell or tissue. It is useful for genome of a molecule in a bovine cell or tissue. It is useful for genome of constructs for use in cattle gene expression, or for genetically the company of the constructs for use in cattle gene expression, or for genetically the complementary has not and the constructs for use in cattle gene expression, or for genetically the complement of the constructs for use in cattle gene expression, or for genetically never the complement of the constructs for use in cattle gene and expression, or for genetically the complement of the constructs for use in cattle gene and expression, or for genetically the constructs of the constructs for the molecule and the constructs for the constructs of the constructs of the constructs of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                       deposition, useful for genome mapping, gene identification and
analysis, cattle breeding, or for genetically improving cattle
                                                                                                                                                                                                                                                                                                                    New nucleic acid associated with lactation, and muscle and fat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
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                                                                                                                                                                                                                                                            Warren WC;
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57.1%; Pred. No. 0.16
ve 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                Claim 2; SEQ ID No 8414; 245pp; English.
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                                                                                                                                                                                                                                                            Tao N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%;
                                                                                                     24-SEP-2001; 2001US-0960352.
                                                                                                                                  12-JAN-1999; 99US-115707P.
                                                                                                                                                                                                                                                         Byatt JC, Mathialagan N,
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                                                                                                                                                                              BYATT J C.
MATHIALAGAN N.
                                                                                                                                                                                                                                                                                       WPI; 2003-110599/10.
                                                                                                                                                                                                              (TAON/) TAO N.
(WARR/) WARREN W C.
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nes 84; Conserv
                                          US2002137139-A1
                                                                         26-SEP-2002
            Bos Taurus.
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                                                            Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (c) assessing the efficacy of a test compound to inhibit prostate
cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid molecule (I) compris a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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Human prostate expression marker cDNA 40054.
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Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                              pharmacogenomic marker; gene; ss.
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25-MAY-2000; 2000US-207454P.
09-UUN-2000; 2000US-21314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
                                                                                                                                                                                                                                                                                                                                                          20-FEB-2001; 2001WO-US05171
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                                                                                                                                                             Homo sapiens.
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147 AAGCAACGCTTGAAAAAGGAAA 169
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18-JUL-2000;
13-DEC-2000;
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Best Local S:
Matches 82
                                                                                                 ABV42105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                         Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assessing the efficacy of a therapy for inhibiting prostate cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      patient; (1) is also useful as a pharmacodyanamic or pharmacogenomic marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 23; Length 556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 556 BP; 389 A; 1 C; 51 G; 113 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61;
                                                                                                                     Human prostate expression marker cDNA 40154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.3;
                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45.4;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 8115; 11750pp; English.
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 34
56 АААААААААААААААААА
                                                     ABV40163 standard; cDNA; 556
                                                                                                                                                                                                                                                                         16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
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                                                                                                                                                                                                                                                                2000US-183319P
                                                                                                                                                                                                                                                                                                        18-JUL-2000; 2000US-219007P
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 57.3
nes 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (a) assessing whether (b) monitoring the pr (c) assessing the eff cancer in a patient, (d) assessing the eff in a patient; (e) selecting a compo (f) assessing the pro (g) determining wheth (h) assessing the agg
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                                                                                                                                                                          Homo sapiens
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                                                                          ABV40163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate expression marker cDNA 42096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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56 AAAAAAAAAAAAAAAAAAAAAAA 34
                                                                                                                                                                                   ABV42105 standard; cDNA; 556
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82; Conservative
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2000US-207454P.
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2000US-219007P.
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
cancer in a patient;
(d) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(ii) a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a

                    cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 TITAIGGGIGAITITIGCTICCTITATATACITITATITATACCCAAATITITICTTAAGC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 464 BP; 199 A; 74 C; 16 G; 116 T; 59 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                      Human prostate expression marker cDNA 3801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 677; 11750pp; English.
                                                                    147 AAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monahan JE;
                                                                                                   AAAAAAAAAAAAAAAAAAAAA 34
                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; cytostati
pharmacogenomic marker; gene; ss.
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16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-21907P.
                                                                                                                                                                                     ABV03810 standard; cDNA; 464
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                                                                                                                                                                                                                     ABV03810;
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ABV03810/
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 បំបើបាប់ប្រជាប់ប្រជាប់ប្រជាប់ប្រជាប់បំបាលបំបាលបំបាលបំបាលបំបាលបំបាលប្រជាប់ប្រជាប់ប្រជាប្រាប្បាល 117
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Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
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    (a) assessing whether a patient is afflicted with prostate cancer;
    (b) monitoring the progression of prostate cancer in a patient;
    (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
    (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                    Human prostate expression marker cDNA 43592
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                                 AAGCAACGCTTGAAAAAAGGAAA 169
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                                                                  AAAAAAAAAAAAAAAAAAAAA
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13-DEC-2000; 2000US-255281P
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                                                                                                                                               ABV43601 standard; cDNA;
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25-MAY-2000;
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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or NA-oligomers for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences
represented in the printed
                                                                                                                                               Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemically treated cell signalling DNA sequence complementary to#45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell signalling; cytosine methylation; cell signalling disease;
cancer; tumour; cytostatic; ds.
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01-SEP-2000; 2000DE-1043826.
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Gaps

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49; Indels

DB 24;

Score 44.6; D Pred. No. 1.1; 0; Mismatches

8.4%;

Query Match Best Local Similarity

74; Conservative

Matches

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The invention relates to 224 nucleic acid sequences comprising at least selected from 43 known genes of complementary sequences). The selected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such diseases, cand therapy of e.g. severe combined immunodeficiency disease, cardiac and therapy of e.g. severe combined immunodeficiency disease, cardiac sathma, HDR syndrome, Sathre-Chotzen syndrome, renal disease, precidancy in the sequence data for this specification and is associated with the human gene regulation-associated genes.

Note: The sequence data for this patent did not form part
                              10323 TTTTTTAAATGGATTTTGAGAATTTATTTTTAAATTTAAATTTAAGTATTTATTGAT 10382
TTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAA 131
                                                                                                                                                                                                                                                                                                                                                             Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Precclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; ososphageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
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                                                                                                                                                                                                                                                                                                                               Human gene regulation-associated gene oligonucleotide #113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 116; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin K;
                                                                                                                                                                                                            AAS61158 standard; DNA; 10988 BP.
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2000DE-1032529.
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                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                              10383 AAA 10385
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WO200179556-A2
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                                                                                                                                                                                                                                                                                              131
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                                                                                                                                                                                                      71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or disclosed are oligonuclecticed suddor bNA oligoners for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction -
                                                                                                                                                                                                                                                  TTATTTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAA
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                                                                                                             DB 24; Length 10988;
                                                                   Sequence 10988 BP; 3128 A; 225 C; 2649 G; 4986 T; 0 other;
                                                                                                                                                       49; Indels
                                                                                                           8.4%; Score 44.6; DE 60.2%; Pred. No. 1.1; ive 0; Mismatches
format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
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01-SEP-2000; 2000DE-1043826.
                                                                                 23-APR-2002 (first entry)
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diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK311545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or their complementary sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       markers for determining the sensitivity of a cancer cell to the anticancer agent TAXOL. Cancer cells can be treated with TAXOL when they are shown to express one of the 242 sensitivity markers or the cells are shown not to express one of the 804 resistance markers. The methods can be used to determine the effectiveness of TAXOL in the treatment of cancer cell growth in an individual. The markers can be used as targets in developing anti-cancer agents such as chemocherapeutic compounds. The markers can also be used as targets in developing treatments for cancer, particularly those cancers which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;
squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
lymphocytic leukaemia; lymphoma; plasmocytoma; reticulum cell sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 ITATTITATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAA
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                                                                                                                                                                                                                                                                                                                                 DB 24; Length 10988;
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Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Van Huffel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cancer agent-sensitive marker #181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 221; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS60450 standard; cDNA; 425 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hodgkin's disease; glioma; ss
                                                                                                                                                                                                                                                                                                                              8.4%;
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                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 60.47
Local Similarity 60.47
Local Similarity 60.47
                                                                                                                                                                                                         European Patent Office
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                                                                                                                                                                                                                                                                                                                                                     display resistance to agents and exhibit expression of the markers. The anticancer agents developed by the novel method can be used to treat cancer. Probes based on the markers can be used to detect transcripts or genomic sequences corresponding to the markers, in the identification of cells or tissues which mis-express the protein. Cancers which may be targeted include carcinoma (e.g. squamous cell carcinoma), asrocma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia), lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's disease and tumours (e.g. glioma). The present sequence is one of the 1046 novel cancer cell markers.
                                                                                                                                                                                                                                                                                                                    70
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pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
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                                                                                                                                                                                                                                                                                    27 TTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAA
                                                                                                                                                                                                                                                       Gape
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                                                                                                                                                                                                                    22; Length 425;
                                                                                                                                                                                                                                                   69; Indels
                                                                                                                                                                                     Sequence 425 BP; 159 A; 41 C; 28 G; 194 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                    147 AAGCAACGCTTGAAAAAGGAAAGTTAGCCCTA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 AAAAAAAAAAAAAAAAAAAAAATTTCCCCCA 163
                                                                                                                                                                                                                      Score 44.4; DB Pred. No. 0.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate expression marker cDNA 10012.
                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABV10021 standard; cDNA; 494 BP
                                                                                                                                                                                                                   ch 8.4%;
1 Similarity 54.9%;
84; Conservative
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16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-21314P.
18-JUL-2000; 2000US-219007P.
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                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                               selecting a composition for inhibiting prostate cancer in a patient, assessing the prostate cell carcinogenic potential of a compound, determining whether prostate cancer has metastasized in a patient, assessing the aggressiveness or indolence of prostate cancer in a
                                                                              assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                27 ITTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAA

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cain a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate call carcinogenic potential of a compou (g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer i

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GA, Ebner R, Komatsoulis G;
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                                                                                                                                                                                                                                                                                      8.4%; Score 44.4; DB 23; Length 494; 59.5%; Pred. No. 0.5; cive 0; Mismatches 51; Indels 0
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                                                                                                                                                                                                                                                    Sequence 494 BP; 299 A; 19 C; 21 G; 155 T; 0 other;
                                                                                                                                                                                                                                                                                                                         51;
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98US-0098634.
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                                                                                                                                                                                                                                                                                                         Local Similarity 59.5
nes 75; Conservative
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P-PSDB; AAY91401.
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31-AUG-1998;
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Matches
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Berlin K;

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Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
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                                                                                                                                                     Claim 1; Page 353; 416pp; English
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Local Similarity 52.8%;
les 93; Conservative 1
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06-APR-2000; 2000DE-1019058.
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and concogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences complementerary to (Sa). The nucleic acid may be a peptide nucleic acide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for a cacertaining genetic and/or epigenetic parameters for the diagnosis a compared to another set of genetic and/or epigenetic parameters in the diagnosis and/or appearance of the present sequence is one of the cifferences serving as basis for diseases and/or epigenetic parameters, the categories diseases are of genetic and/or epigenetic and/or epigenetic and/or epigenetic parameters which are disadvantageous to patients. The present sequence is one of the correspondences sequences derived from tumour suppressor genes and compared sequence of the corresponding odd numbered sequence (e.g. componences with even numbered Seq ID numbered sequence (e.g. componences and IDI, ID 536 and ID 535, except for those whose partner sequence
                                                                                                                                                                                                                                                                                                                      Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 128; 27pp; English
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                              Piepenbrock C,
                                                                                                                              (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                               WPI; 2001-602752/68.
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                                                                                                                                                                                           olek A,
   human secreted proteins given in AAY91346 to AAY91449. The human secreted proteins given in AAY91346 to AAY91449. The human secreted proteins given in AAY91346 are neuroprotective; motoropic; proteins can have activities based on the tissues and cells they are revpressed in Examples of the activities are: neuroprotective; nootropic; neuroleptic; antimmaic; cerebroprotective; immunomodulatory; anti-microbial; cardiant; cytostatic; antiinflammatory; haemostatic; anticonvulsant; and vasotropic. The polynocleotides and proteins may be used to prevent, treat or ameliorate a medical condition, e.g. by protein or gene therapy. Conditions treatable by the proteins of the invention or gene therapy. Conditions treatable by the proteins of the invention include neural, reproductive, or immune disorders, especially immunodeficlency, infection, lymphomas, demyelinating diseases, auto-immunities, cancer, general microbial infection, inflammation, aneuvymms and haemorrhages. Specific examples include: Alzheimer's disease; Parkinson's; Huntingon's; Tourette syndrome; multiple sclerosis; meningitis; ischaemais; Prostate cancer; mania; dementa; obsessive compulsive disorder and viral prophylaxis. The polynucleotides and proteins can also be used in the detection of disorders associated with the function of the protein, the disorders of the developmental alsorders, sexually-linked disorders of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiovascular system. They may also be used as food additives or preservatives. AAA26272 to AAA26280 and AAY91345 are sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide sequences given in AAA26281 to AAA26336 encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                              Novel secreted proteins and corresponding DNA molecules that can be used to prevent, treat and diagnose disease in humans, for example, Alzheimer's, cancer, and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44.4; DB 21; Length 664;
Pred. No. 0.55;
1; Mismatches 82; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 664 BP; 206 A; 138 C; 133 G; 182 T; 5 other;
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4435
                                                                                                                                                                       ö
                                                                                      65 TATACTTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAAT 124
                                                                                                                   125 TATCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGG
                                                        Gaps
                                                          °
                          / Match 8.4%; Score 44.4; DB 22; Length 6078; Local Similarity 54.4%; Pred. No. 1.1; hes 87; Conservative 1; Mismatches 72; Indels 0;
Sequence 6078 BP; 1615 A; 218 C; 1499 G; 2746 T; 0 other;
                                                                                                                                                                                                                              Human immune system associated gene SEQ ID NO: 1110.
                                                                                                                                                                                                              185 TATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTCTA
                                                                                                                                                                                                                                                                                                                     ABL33137 standard; DNA; 6078 BP
                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                   ABL33137;
                                                           Matches
                                                                                                                                                                                                                                                                                       RESULT 31
                                                                                                                                                                                                                                                                                                        ABL33137,
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The sequence represents a cervical cancer pre-malignant condition marker.

These markers encode proteins that are over expressed during
tumourigenesis. The proteins and their corresponding nucleic acid
sequences can therefore be used for the diagnosis, prevention and
readment of cervical cancers, particularly cervical intraepithelial
coplasia (CIN) and squamous intraepithelial lesions (SIL). The sequences
may be used as markers in diagnostic assays to detect cancerous
conditions (e.g. by polymerase chain reaction (PCR) or enzyme linked
immunosorbent assay (ELISA), to monitor the efficacy of anticancer
therapies and to identify anticancer or carcinogenic compounds. The level
cervicals of expression of the marker in a patient sample is compared with the normal
level of expression of the marker in a control non-cervical cancer
sample, whereby a significant difference indicates that the patient is
afflicted with cervical cancer or a pre-malignant condition. The
cervical cancers. They may be used in this way for the treatment
cervical intraepithelial neoplasia or squamous intraepithelial
                                                                                                                                                                                                                                                                                                                                                                                                                               Cervical cancer protein markers useful for the diagnosis, prevention and treatment of cervical cancers, especially cervical intraepithelial neoplasia or squamous intraepithelial lesions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITATATGCTGATTTATGGGTGATTTTTGCTTCCTTCTTTATACTTTTATTTTATTCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22; Length 198;
anticancer therapy; carcinogen; antisense inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 198 BP; 67 A; 11 C; 10 G; 102 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43.8; DB Pred. No. 0.53; 0; Mismatches
                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 AAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABX47018 standard; cDNA; 236 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Page 407; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.3%;
llarity 54.5%;
Conservative
                                                                                                                                                                                                              14-MAR-2000; 2000US-0189113.
31-MAR-2000; 2000US-0193943.
12-MAY-2000; 2000US-0203772.
                                                                                                                                           08-DEC-2000; 2000WO-US33311.
                                                                                                                                                                                                                                                                      2000US-0210820
                                                                                                                                                                                                                                                                                     21-JUL-2000; 2000US-0220113
                                                                                                                                                                                                                                                                                                                                                            Deeds J,
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-367889/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 78; Conserv
                                                                      WO200142792-A2
                                     Homo sapiens.
                                                                                                                                                                                                21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                            Schlegel R,
                                                                                                          14-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
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Matches
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ID ABX4
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AC ABX4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid relukaemia, Alzheimer's disease, Alzheitepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4434 AAAAAAAAAAAAAAACHTTAAAACCATTTTT 4375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 TATACTTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATAAAT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 TATCAAAAGAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cervical cancer; pre-malignant condition marker; tumourigenesis; CIN; ds; cervical intraepithelial neoplasia; squamous intraepithelial lesions; polymerase chain reaction; PCR; enzyme linked immunosorbent assay; ELISA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
system disease; cytosine methylation; antiasthmatic;
              antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer, eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.4%; Score 44.4; DB 24; Length 6078; 54.4%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1110; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6078 BP; 1615 A; 218 C; 1499 G; 2746 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4374 TATTTTTTATATTTTTAATATTTTCCAAATTTTCTACAA 4335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cervical cancer pre-malignant condition DNA marker #26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTCTA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 54.4%;
es 87; Conservative
                                                                                                                                                                                                                                                                   02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                      30-JUN-2000; 2000DE-1032529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS07727 standard; DNA; 198
                                                                                                                                                                                                                                                                                                                                                                                            Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-130909/17.
                                                                                                                                                                                                WO200200928-A2
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                   03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185
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                                                                                                                                                                                                                                                                                                                                                                                              Olek A,
                                                                                                                            dene;
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Matches
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Indels

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is a afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient,
(c) assessing the efficacy of a test compound to inhibit prostate 107 iriririririrrirririringgaarariaaahaahaahaahaahaaaaaaaaaa 166 cancer; cytostatic; carcinogen; pharmacodyanamic marker; marker; gene; 88. (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer ö Match 8.3%; Score 43.8; DB 23; Length 323; Local Similarity 53.3%; Pred. No. 0.62; Local Similarity 63.0% Mismatches 79; Indels 0; Sequence 323 BP; 109 A; 58 C; 34 G; 120 T; 2 other; Human prostate expression marker cDNA 60987. (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. Claim 1; Page 11593; 11750pp; English. 147 AAGCAACGCTTGAAAAAAGGAAA 169 Schlegel R, Endege WO, Monahan JE; BP 2000US-211314P. 2000US-211314P. 2000US-219007P. ABV60996 standard; cDNA; 323 20-FEB-2001; 2001WO-US05171 2000US-255281P (first entry) Human; prostate cancer; pharmacogenomic marker; WPI; 2001-662795/76. WO200160860-A2. in a patient; Homo sapiens. 13-DEC-2000; 17-FEB-2000; 16-MAR-2000; 25-MAY-2000; 09-JUN-2000; 23-AUG-2001. 18-JUL-2000; 13-SEP-2002 ABV60996; Query Match patient Matches RESULT 34 ABV60996 ò 셤 ò invention relates to a purified nucleic acid molecule associated with 86 Bovine; 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding. TITATATATGCTGATTITATGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTTATTCCCAAA Bovine EST associated with lactation/muscle/fat deposition #12183 Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: ö New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle Score 43.8; DB 25; Length 236; Pred. No. 0.56; 0; Mismatches 62; Indels 0 seqdata.uspto.gov/sequence.html?DocID=20020137139. Sequence 236 BP; 63 A; 13 C; 23 G; 137 T; 0 other; 62; nucleic acids. Warren WC; Claim 2; SEQ ID No 12183; 245pp; English. (expressed sequence tag) Tao N, 8.3%; 12-JAN-1999; 99US-115707P. 11-JAN-2000; 2000US-0480902. 24-SEP-2001; 2001US-0960352. 21-FEB-2003 (first entry) Byatt JC, Mathialagan N, 81; Conservative (BYAT/) BYATT J C. (MATH/) MATHIALAGAN N. WPI; 2003-110599/10. (TAON/) TAO N. (WARR/) WARREN W C. Local Similarity US2002137139-A1. 26-SEP-2002. Bos Taurus. Query Match LMFD EST Matches

ö 63 Gapa is also useful as a pharmacodyanamic or pharmacogenomic marker.

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180 riticitatitagairitairicittairiticciticaitaaagrairittataaraaaaaaa 239

123 ATTATCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAA 169

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymptodies are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hemmatopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                  64 TTATACTTTTATTTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAA 123
                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                            124 TTATCAAAAAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTT 172
                                                                                                                                               136 CCCCCAAAAAAAAAAATTTTTCCCCCCCCAAAAAAATTTT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 10923; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 378 BP; 148 A; 35 C; 62 G; 133 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                         Human polynucleotide SEQ ID NO 10923.
                                                                                                                                                                                                                                           AA190863 standard; cDNA; 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                    (first entry)
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P-PSDB; AAO10932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                  06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders
                                                                       92
                                                                                                                                                                                                                                                                                 AA190863;
                                                                                                                                                                                                      RESULT 35
                                                                                                                                                                                                                           AAI90863
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                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 8655; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 411 BP; 214 A; 24 C; 64 G; 107 T; 2 other;
                                                                                                                          Human polynucleotide SEQ ID NO 8655.
                 ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT, Liu C, Drmanac RT;
                 AAI88595 standard; cDNA; 411
                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001; 2001WO-US04927.
                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-514838/56.
P-PSDB; AAO08664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                            WO200164835-A2
                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                       06-NOV-2001
                                                                                                                                                                                                                                                                                                                                07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders
                                                     AA188595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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AA188595,
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Gaps

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Match 8.3%; Score 43.8; DB 22; Length 378; Local Similarity 53.9%; Pred. No. 0.64; les 90; Conservative 0; Mismatches 77; Indels 0.

Query Match Matches

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The invention relates to a nucleic acid comprising a sequence (I) of at least 18 bases in length of a segment of chemically pre-treated genomic DNA which has any one of the sequences of (ARX33919-ARX3403) or its complement. Also included are an oligomuclectide or peptide nucleic acid (or set thereof) of at least 9 nucleotides which hybridises to (I), probes for detecting cytosine methylation or singlenchelotide polymorphisms (SNP) in (I), a marray of oligomers or peptide nucleic acids for analysing diseases associated with the nucleotide polymorphisms (SNP) in (I), a marray of oligomers or peptide nucleic acids for analysing diseases associated with the correction of the CpG dinucleotides of (I). The array is useful for determining genetic and/or epigenetic parameters, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas, or the predisposition to astrocytomas paralysing cytosine pastrocytomas, or the predisposition to astrocytomas paralysing genemic CDNA, extracting the genomic DNA, extracting the genomic DNA, converting cytosine bases which are unmethylated at the 5-position, in the genomic DNA sample, to uracil or another base which is dissimilar to cytosine in terms of hybridisation cancther base which is dissimilar to cytosine positions by reference to amplificates carry a detectable label. The method further involves denetifying methylation status of one or more cytosine positions by reference to canalysing methylation status of the cytosine positions by reference to come or more data setts. The genomic DNA is chemically treated by using a bising methylation status of the cytosine positions by reference to come or more data setts. The genomic DNA is chemically treated by using a bisulphite, hydrogen sulphite or disalphite. The amplification or more data setts of the cytosine positions by using a bisulphite, hydrogen sulphite or disalphite. The amplification or recorrections or recorrections and setting methylator or step amplification or step amplificates carry and 
                                             71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, ds, astrocytoma, cytostatic, staging, cysteine methylation, CpG, bisulphite, brain tissue, MALDI, ESI, electron spray mass spectrometry; matrix assisted laser desorption/ionization mass spectrometry.
                                                                                               Novel chemically modified genomic DNA sequences, useful in the characterisation, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas or predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DNA for staging of Astrocytomas #4.
                                                                                                                                          147 AAGCAACGCTTGAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 7; 37pp; English.
                                                                                                                                                                                         10 AAAACCAAAAAAAAAAAAAA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berlin K;
                                                                                                                                                                                                                                                                                                             ABK33925 standard; DNA; 9884 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-2001; 2001WO-EP07538
                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG
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brain tissue, based on the specific genomic methylation status of brain tissues, as opposed to background DNA. The amplificates carry a fluorescent label or radionuclide. Obtionally, the labels of the amplificates are detachable molecule fragments having a typical mass which are detected in a mass spectrometer. The fragments of chemically pre-treated genomic DNA to be amplified, have a single positive or negative charge for a better detectability in the mass spectrometer. Preferably, the amplificates or fragments of the amplificates are detected by matrix assisted laser desorption/ionization mass spectrometry (MALDI) or using electron spray mass spectrometry (MALDI) or using electron spray mass spectrometry (SSI). The samples of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                       66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                     40 TTAIGGGIGATITIGCTICCTICTITATACTITIATITICCCAAATTTTTAAGCA
                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour suppressor gene derived chemically modified sequence #519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.3%; Score 43.8; DB 24; Length 9884; 62.2%; Pred. No. 1.7; ive 0; Mismatches 42; Indels 0;
                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                   Sequence 9884 BP; 2483 A; 226 C; 2338 G; 4837 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 519; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS46793/c
ID AAS46793 Btandard; DNA; 56153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAR-2001; 2001WO-EP02955.
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07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                   69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200168912-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes and
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                   Matches
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16-MAR-2000; 2000US-189862P

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Dases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a segment to the from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences complementary to (58). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may for many part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters may be compared to another set of genetic and/or epigenetic parameters which are disadvantageous to patients. The present sequence is one of the are disadvantageous to patients. The present sequence is one of the season of the compared compared to another set of genetic and/or epigenetic parameters which are disadvantageous to patients. The present sequence is one of the season of the compared compared to another set of compared to another set of genetic and/or epigenetic parameters which are disadvantageous to patients. The present sequence is one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39861 TCTATCAATTTTTATTTAACCCAATTACCTATAATCAAATAAAATTTTCATTCTTTAAAT 39802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39801 ACTTTTATACAATAATCATAATAAACACATACTCCTTAAATTTTTATTCATTTAAAAA 39742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39681 TCTTTTAAAATAAAAACTCGCTCTATCACCCAAACTAAAATTACAATAACGCGATCTCAA 39622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 TITIATACTITITATITACCCAAATITITICTIAAGCAAATATITCTTIGCTAATAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 TCTTTGAGCAGGAAAGAAAAGCAGTCACCCTCTCTTCCATGACAACAACCATGACCGG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 GGTATATTTTGGAAGTTGTAAAATACTACRIGTTCTCTTTCTAAGTCCCACTCCTCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 56153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56153 BP; 13943 A; 1002 C; 14095 G; 27113 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43.8; DB 22;
Pred. No. 2.8;
1; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate expression marker cDNA 60932.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39621 Crcacracaaccrccarcrccaa 39597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCTTGCCTGCTCCATCACAGGAA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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Best Local Similarity 47.5%;
Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          oncogenes.
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comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                               selecting a composition for inhibiting prostate cancer in a patient, assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                               prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 ITTAIAIGCIGAITIAIGGGIGAITITIGCITICCITITIAIACITITAITIAITICCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid molecule (I) compa nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.2%; Score 43.6; DB 23; Length 626;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 626 BP; 356 A; 15 C; 41 G; 130 T; 84 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune system associated gene SEQ ID NO: 1449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.84;
0; Mismatches
                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 AAGCAACGCTTGAAAAAAGGAAAGTT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 11585; 11750pp; English.
                                                                                                                                 Monahan JE;
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             25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
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                                                              13-DEC-2000; 2000US-255281P.
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                                                                                                                                                                WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               in a patient;
(e) selecting
(f) assessing
(g) determinir
(h) assessing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patient
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Homo sapiens.

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Bovine, ss; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABX46053 standard; cDNA; 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-1999; 99US-115707P, 11-JAN-2000; 2000US-0480902.
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                                                               Schlegel R, Deeds J,
                                                                                     WPI; 2001-375006/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BYAT/) BYATT J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2002137139-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos Taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX46053;
                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1088 tricinicrininininintrininininininininininaananniaancahichaaa 1029
                                                                                                                                                                                                                                        The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, necvascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheimer's disease, Alzheimer's disease, and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                              TITATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                  DB 24; Length 6590;
                                                                                                                                                                                                                                                                                                                                             Sequence 6590 BP; 2030 A; 155 C; 1534 G; 2871 T; 0 other;
                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1449; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                       59; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cervical cancer marker nucleic acid 1323
                                                                                                                                                                                                                                                                                                                                                                8.2%; Score 43.6; DE
Local Similarity 57.2%; Pred. No. 1.7;
Nes 79; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGCAACGCTTGAAAAA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATAAACACGTAAACAAA 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH70049 standard; cDNA; 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1999; 99US-0169681.
21-DEC-1999; 99US-0171350.
14-MAR-2000; 2000US-0189315.
                                                                        30-JUN-2000; 2000DE-1032529.
                                                   02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-DEC-2000; 2000WO-US33312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-SEP-2001 (first entry)
                                                                                                                              Piepenbrock C,
                                                                                                          (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                cytosine methylation
                                                                                                                                                    WPI; 2002-130909/17.
          WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200142467-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUN-2001
                               03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       896
                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH70049
                                                                                                                             olek A,
                                                                                                                                                                                                                                                                                                                                                                                       datches
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183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is affiliated with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 TTATCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGG
                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 TIATACTITIATITATICCCAAATITITCTTAAGCAAATATTTCTTTGCTAATCAATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
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Pred. No. 0.75;
0; Mismatches 106; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 300 BP; 81 A; 27 C; 20 G; 143 T; 29 other;
                                                                                                                                    (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTTTTTAAGGGAAAAAAAAAA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTATATTTTGGAAGTTGTAAAATA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1, Page 309; 1051pp; English
                                                                                                                                                                                                           Berger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.2%;
48.0%;
12-MAY-2000; 2000US-0203791.
09-JUN-2000; 2000US-0210600.
21-JUL-2000; 2000US-0220114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 48.0 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for gene therapy.
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63 84 123

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Human prostate expression marker cDNA 4390
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                                                                                                                                 WO200160860-A2
                                                                                                                                                                                                                                          17-FEB-2000; 2
16-MAR-2000; 2
25-MAY-2000; 2
09-JUN-2000; 2
                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in a patient;
                                                                                                                                                                                                                                                                                                                                         13-DEC-2000;
                                                                                                                                                                    23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABX44170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patient
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (£)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABX44170
   SXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                      The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide comprising any particle acid molecule comprising any of 15112 nucleotide comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that functions in the cell to cause termination of translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end compression and addition of polyadenylated ribonucleotides to a 3' end complement or fragment) with a complementary nucleic acid sequences or its nucleic acid (comprising any of the 15112 nucleic acid molecule complement or fragment) with a complementary nucleic acid molecule complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid is predictive of the level or pattern of the complementary nucleic acid is predictive of the level or pattern of the nucleic acid is predictive of the level or pattern of the molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically more recomplements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 TIATACTITIAITTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATAAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .24 TTATCAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAAGGAAAGTTAGCCCTATCGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence was not shown in the specification but otained in electronic format from the USPTO web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                   and muscle and fat identification and
                                                                                                                                                                      deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43.4; DB 25; Length 424; Pred. No. 0.83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 GTATATTTTGGAAGTTGTAAAATACTACRTGTTCTCTTTTAAG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 ATTITAAATATITGITTAAAATATAAAAAAAAAAAATATATAAG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         segdata.uspto.gov/sequence.html?DocID=20020137139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 424 BP; 228 A; 7 C; 32 G; 157 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (expressed sequence tag) nucleic acids.
                                                                           Warren WC;
                                                                                                                                                   New nucleic acid associated with lactation,
                                                                                                                                                                                                                           Claim 2; SEQ ID No 11218; 245pp; English.
                                                                           Tao N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABV04399 standard; cDNA; 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was obtained in electronic
                                                                         Mathialagan N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 49.3
Matches 110; Conservative
(MATH/) MATHIALAGAN N.
                     (TAON/) TAO N.
(WARR/) WARREN W C.
                                                                                                              WPI; 2003-110599/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-SEP-2002
                                                                           Byatt JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV04399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMFD EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 43
ABV04399/C
ID ABV043:
XX
AC ABV043:
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147
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Human, prostate cancer, cytostatic, carcinogen, pharmacodyanamic marker, pharmacogenomic marker, gene, 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 TINITTTTTTTTTTANNGGINTTTTTTTTTTNNATTTTTANCNTTNTTTTTTTTTTT

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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2.1%; Pred. No. 0.83;
ve 0; Mismatches 68; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 431 BP; 139 A; 63 C; 34 G; 114 T; 81 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schlegel R, Endege WO, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 762; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 AGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAAAAAAAAAAAA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABX44170 standard; cDNA; 380 BP
                                                                                                                                                                                                                                                                                                                                                                                         , 2000US-183319P.
, 2000US-189862P.
, 2000US-207454P.
, 2000US-211314P.
, 2000US-219007P.
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                                                                                                                                                                                                                                                                                                                           20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-255281P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 52.1 tes 74; Conservative
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Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site:
                  Bovine BST associated with lactation/muscle/fat deposition #9335.
                                                                                                                                                                                                                                                                             deposition, useful for genome mapping, gene identification and
analysis, cattle breeding, or for genetically improving cattle
                                                                                                                                                                                                                                                                New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 380 BP; 154 A; 22 C; 46 G; 158 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         segdata.uspto.gov/sequence.html?DocID=20020137139.
                                                                                                                                                                                                                                                                                                      Claim 2; SEQ ID No 9335; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (expressed sequence tag)
                                                                                                                                                 12-JAN-1999; 99US-115707P.
                                                                                                                                24-SEP-2001; 2001US-0960352.
21-FEB-2003 (first entry)
                                                                                                                                                                                                                            Byatt JC, Mathialagan N,
                                                                                                                                                                            BYATT J C.
MATHIALAGAN N.
                                                                                                                                                                                                                                               WPI; 2003-110599/10.
                                                                                                                                                                                                          (WARR/) WARREN W C.
                                                                                            US2002137139-A1.
                                                                                                              26-SEP-2002.
                                                                         Bos Taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LMFD EST
                                                                                                                                                                              BYAT/)
                                                                                                                                                                                       MATH/)
                                                                                                                                                                                                 (TAON/)
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Warren WC;

Tao N,

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(b) any one of 115 polynucleotide sequences (ABV83558-ABV83672);
(c) a molecule that selectively hybridizes to (a) or (b);
(d) a molecule having at least 60% sequence identity to (a) or (b).

The breast specific nucleic acid of sequence identity to (a) or (b).

The breast specific nucleic acid of sequence identity is maging and treating breast cancer and non-cancerous disease states in breast tissue. They are also useful for producing transgenic animals and cells and producing engineered breast tissue transgenic animals are useful as animal model systems used in elaborating
                       109 TITITITITATAAAAATATITITCAAATITAAAAAATATAATTGITTAAAATTITITI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the biological function of the polypeptides, studying conditions and/or disorders associated with aberrant expression and in screening for compounds effective in ameliorating the conditions. The polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 TITTGCTTCCTTTATACTTTTATTCCCAAATTTTTCTTAAGCAAATATTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; breast; cytostatic; cancer; transgenic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated breast specific nucleic acid molecules and polypeptides, useful for identifying, diagnosing, monitoring, staging, imaging and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for identifying, diagnosing, monitoring, staging, immging etrating breast cancer and non-cancerous disease states in breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cafferkey R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human breast specific nucleic acids (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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llarity 60.0%; Pred. No. 0.93;
Conservative 0; Mismatches 48; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (a) a sequence encoding any one of 95 protein sequences (ABP66614-ABP66708);
Hu P, Recipon H, Karra K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 430 BP; 135 A; 97 C; 103 G; 95 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are useful for gene therapy and in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                            Human breast specific gene SEQ ID NO 87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 193-194; 254pp; English.
                                                                                                                             169 AAAAAAATTAAAAAAAAAAAA 192
                                                                             147 AAGCAACGCTTGAAAAAGGAAAG
                                                                                                                                                                                                                                                       ABV83644 standard; cDNA; 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-FEB-2002; 2002WO-US04284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L5-FEB-2001; 2001US-268999P
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S, Macina RA,
Liu C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DIAD-) DIADEXUS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-713345/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200266605-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                            06-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising:
                                                                                                                                                                                                                                                                                                          ABV83644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sun Y,
                                                                                                                                                                                                                                  ABV83644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a purified mucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD incleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as BRX34836-ABX49947, or complements of them. Also included are; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' nontranslated sequence that functions in the cell to cause termination of translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the molecule in a bovine cell or tissue comprising; (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its oncleic acid (comprising any of the 15112 nucleic acid sequence or its complement or fragment) with a complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid and the complementary nucleic acid is predictive of the lavel or pattern of the complementary nucleic acid is used for detecting the level or pattern of the complementary nucleic acid is used for determining a level or pattern of the mapping, gene identification and analysis, cattle breeding, preparation of mapping, gene identification and analysis, cattle breeding, preparation of the present sequence is one of the 15112 bovine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98
                                                                                               Bovine; 88; EST; expressed sequence tag; lactation; LMFD; muscle deposition; fat deposition; genome mapping; gene identification; gene analysis; cattle breeding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 ITTAIAIGCIGAITTAIGGGIGAITTIGCIITCCIITCITIAIACTITIAITAITCCCAAA
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nucleic acids.

8.2%; Score 43.2; DE 56.2%; Pred. No. 0.9; iive 0; Mismatches

81; Conservative

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Local Similarity

Matchea

Query Match

109 111

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Search completed: February 14, 2004, 14:10:12 Job time : 285 secs

Sequence 36, Appl Sequence 38, Appl Sequence 36, Appl Sequence 4, Appl Sequence 1, Appl Sequence 208, App Sequence 208, App Sequence 208, App Sequence 208, App Sequence 2, Appl	1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	, , , , , , , , , , , , , , , , , , ,	sequence 10, Appl Sequence 11, Appl Sequence 12, Appl Sequence 13, Appl Sequence 12, Appl Sequence 14, Appl Sequence 46, Appl Sequence 46, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 10, Ap
US-08-747-221B-36 US-08-747-221B-38 US-09-005-051-38 US-09-005-051-38 US-09-005-651-4 US-09-234-245-1 US-09-234-245-1 US-09-24-1-208 US-09-618-166-208 US-09-894-731-2		US-08-484-106-17 US-09-333-214-3 US-09-628-18-3 US-09-367-895-29 US-08-981-803-29 US-08-981-403-29 US-09-904-615-59 US-09-328-111-147 US-09-328-111-147 US-09-328-111-147 US-09-328-111-147 US-09-328-111-147 US-09-328-111-147 US-09-331-9 US-08-461-809-9 US-09-193-707-4 US-09-193-707-4 US-09-193-707-4 US-09-193-707-4 US-09-193-707-4 US-09-193-707-4 US-09-193-707-6 US-09-193-707-6 US-09-193-707-6 US-09-193-707-6 US-09-193-707-6 US-09-193-707-6 US-09-193-707-6 US-09-193-707-6 US-09-193-707-6 US-09-193-707-6	US-08-781-420-10 US-08-781-420-10 US-08-781-420-12 US-08-874-102-12 US-09-006-595A-10 US-09-006-595A-10 US-08-984-919A-46 US-08-984-919A-46 US-08-984-919A-46 US-08-984-919A-46 US-08-984-919A-46 US-09-620-312D-706 US-09-620-312D-706 US-09-725-284-1 US-09-725-359A-1 US-09-725-359A-1 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-112 US-09-149-476-110 US-08-990-571-10 US-08-990-571-10 US-08-950-571-10 US-08-950-571-10
2007 3 2007 3 2007 3 2007 3 2007 3 2334 1 3715 4 6442 4 1037 4 4140 3		70774440111110000444	1044472 3 7 11 11 11 11 11 11 11 11 11 11 11 11 1
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n 5.1.6 Compugen Ltd. search time 71 Seconds (without alignments) 3288.615 Million cell undates/sec	tgag 529	eq:* eq:* eq:* leq:* leq:* la.seq:* l.seq:* l.seq:* idistribution. bescription	Sequence 66, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 11, Appli Sequence 11, Appli Sequence 20, Appl Sequence 24, Appl Sequence 24, Appl Sequence 34, Appli Sequence 34, Appli Sequence 31, Appli Sequence 31, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 5, Appli Sequence 6, Appli Sequence 11, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compug nucleic search, using sw model February 14, 2004, 13:57:05 ; Searc	1 3tagtcgt spext 1.0 20691566 residues 3 chosen paramete	Maximum Match 100\$ Listing first 100 summaries Issued Patents NA:* 1: /cgn2_6/ptodata/2/ina/5B_COMB.seq:* 2: /cgn2_6/ptodata/2/ina/6B_COMB.seq:* 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:* 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:* 5: /cgn2_6/ptodata/2/ina/6B_COMB.seq:* 5: /cgn2_6/ptodata/2/ina/A_COMB.seq:* 6: /cgn2_6/ptodata/2/ina/A_COMB.seq:* 6: /cgn2_6/ptodata/2/ina/A_COMB.seq:* 7: /cgn2_6/ptodata/2/ina/A_COMB.seq:* 6: /cgn2_6/ptodata/2/ina/A_COMB.seq:* 7: /cgn2_6/ptodata/A_COMB.seq:* 7: /cgn2_6/ptodata/A_COMB.seq:* 7: /cgn2_6/ptodata/A_COMB.seq:* 7: /cgn2_6/ptodata/A_COMB.seq:* 7: /cgn2_6/ptodata/A_COMB.seq:* 7: /cgn2_6/ptodata/A_COMB.seq:* 7: /cgn2_6/ptodata/A_COMB.seq:*	8.4 664 4 US-07-08-07-106-2 8.6 2672 1 US-08-09-04-615-66 8.0 2672 1 US-08-09-04-18-9 7.5 1342 4 US-09-187-999-14 7.5 8920 2 US-08-187-999-14 7.5 8920 2 US-08-18-19-11 7.5 664 4 US-09-187-999-14 7.3 1378 4 US-09-149-476-20 7.3 2323 3 US-09-149-476-20 7.3 5232 3 US-09-149-476-20 7.3 5232 3 US-09-149-476-20 7.3 5232 3 US-09-149-476-20 7.3 5232 3 US-09-149-476-20 7.3 5232 3 US-09-149-476-20 7.4 1582 3 US-08-149-476-66 7.5 1582 3 US-08-149-476-66 7.7 1 5656 4 US-09-410-464-5 7.1 3828 4 US-09-21-0138-165 7.1 3828 4 US-09-21-0138-165 7.1 1664976 4 US-09-21-0138-165 7.1 1664976 4 US-09-1869-16-2 7.0 1582 1 US-09-1869-16-2 7.0 1582 1 US-09-1869-16-2 7.0 1582 3 US-08-545-1968-10

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72 TTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCAAA 131
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One Liberty Place 46th Floor
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Sequence 2, Application US/07867106 ·
Patent No. 5389526
GENERAL INFORMATION:
APPLICANT: Chang, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 AGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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2378..5038
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2378..5038
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ADDRESSEE: Woodcock 1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                     Philadelphia
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                                                                                                                                                                                                                                                                                                                 USA
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ANTI-SENSE: NO
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LOCATION:
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US-07-867-106-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                             STREET:
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147 AAGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGGTATTTTGGAAGTTGTA 202
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52.8%; Pred. No. 0.006;
tive 1; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08703947
Patent No. 5788962
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wise, Kim S.
APPLICANT: McIntosh, Mark A.
TITLE OF INVENTION: DNA Sequences Coding for Mycoplasma
TITLE OF INVENTION: Hyppneumoniae Surface Antigens,
TITLE OF INVENTION: Corresponding Proteins and Use in
TITLE OF INVENTION: Vaccines and Diagnostic Procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 63043

CMDUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage COMPUTER: Hewlett-Packard Vectra
OPERATING SYSTEM: MS-DOS Version 3.3
                                                                          APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: P2032P1
CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
FRIOR APPLICATION NUMBER: 09/511,554
FRIOR PILING DATE: 1990-08-25
FRIOR FILING DATE: 1990-08-25
FRIOR FILING DATE: 1990-08-31
FRIOR FILING DATE: 1990-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PATCHIN VET: 2.0
SEQ ID NO 66
LENGTH: 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
LOCATION: (63)
OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Grace J. Fishel
STREET: 929 Fee Fee Road, Suite 100
                Sequence 66, Application US/09904615
Patent No. 6566325
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 52.8
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: SITE
LOCATION: (31)
OTHER INFORMATION: n equ
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Grace J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                St. Louis
Missouri
Y: USA
JS-09-904-615-66/c
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STATE: M:
COUNTRY:
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1281 Tritiririrrrrrrrrrrrrrrrrrcgaaraarrarrrrrraacagararaaaar 1222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340 TTAAGAATTTTCTTGCTTTTTTCTTCATAATTTTTCCTTTTTCTATATTTTTTGATGG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 TITATATGCTGATITATGGGTGATITITGCTTCCTTCTTTATACTTTTATTTCCCAAA 86
                                                                                                                                                                                                                                                                                                                                         40 TTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTCCCAAATTTTTCCTTAAGCA 99
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                                                                                                                                                                                          Score 42.4; DB 1; Length 2672;
Pred. No. 0.04;
0; Mismatches 76; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 AAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 AAAATCAACAAGATTTTTATATTTTCTAAATTAAATTCAAAA 177
                                FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: From 1 to 2672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Rosen et al
ITILE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P1
CURRENT APPLICATION NUBER: US/09/489, 847
CURRENT FILING DATE: 2000-01-24
EARLIER FILING DATE: 1999-07-29
EARLIER FILING DATE: 1999-07-29
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER RILING DATE: 1998-08-05
EARLIER RILING DATE: 1998-08-06
EARLIER RILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
SARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SOFTWARE: PAREIT VALUE OF THE OF
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Patent No. 6476195
                                                                                                                                                                                                        8.0%;
                                                                                                                                                                               Query Match
Best Local Similarity 53.7%
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-489-847-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 ACTACRTG 214
DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
US-09-489-847-89/c
                                                                                                                                    US-08-703-947-1
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NAME/KEY: the structural gene for the surface lipoprotein
NAME/KEY: bc and includes 312 bp upstream and 479
NAME/KEY: bp downstream of coding sequence
LOCATION: coding sequence for P65 spans 1881 bp of
LOCATION: includes all sequence (begins at nt 313 and
LOCATION mircludes all sequence through nt 2193)
IDENTIFICATION METHOD: frame; by similarity to pattern of open reading
IDENTIFICATION METHOD: sequence with immune serum to P65
OTHER INFORMATION: immunogenic surface lipoprotein of no known
OTHER INFORMATION: function; C-terminus exposed on external
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CELL.
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY: Genomic in Charon 4A, GEM12
LIBRARY: Genomic in Charon 4A, GEM12
CLONE: MhpJ25, MhpJ35, MhpJG35, pZJ25, pZJ25.1, pZ125.14,
CLONE: PZJG35.1, pZJG35.12, pZJG35.13, pZJG35.14
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Expressed in Escherichia coli from a Cloned
Genomic Fragment
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AUTHORS: Mary F. Kim, Manijeh B. Heidari, Susan J. AUTHORS: Mary F. Kim, Manijeh B. Heidari, Susan J. AUTHORS: Stull, Mark A. McIntosh, and Kim S. Wise TITLE: Identification and Mapping of an TITLE: Immunogenic Region of Mycopleama TITLE: hyopneumoniae p65 Surface Lipoprotein TITLE: hypopneumoniae p65 Surface Lipoprotein TITLE: Appresed in Escherichia coli from a Cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHROMOSOME/SEGMENT: single chromosome
MAP POSITION: unknown
UNITS: unknown
                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,947
FILING DATE: 28-AUG-1996
CLASSIFFICATION NATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/373,957
FILING DATE: January 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Fishel, Grace J.
REGISTRATION NUMBER: 25864
REFERENCE/DOCKET NUMBER: UVM 8141
TELECHONE: (314) 878-0440
TELECHONE: (314) 275-7693
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STRAIN: J
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CELL TYPE: unicellular bacterium
CELL LINE:
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DESCRIPTION: region of 5.8 kd
DESCRIPTION: genomic library
HYPOTHETICAL: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 2572 Dase pairs TYPE: nucleic acid STRANDEDNESS: single
SOFTWARE: WordPerfect 5.1
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DATE: August 1990
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FRAGMENT TYPE:
ORIGINAL SOURCE:
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SEQUENCE CHARACTERISTICS:
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                                                                                                               US-08-446-855A-1
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                                                                                                                                                       Query Match
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                                       Sequence 14, Application US/09187999A

Sequence 14, Application US/09187999A

Patent No. 6482646

GENERAL INFORMATION:
APPLICANT: Gindullis, Frank
APPLICANT: Gindullis, Prank
APPLICANT: Gindullis, Prank
APPLICANT: Moier, Iris
TITLE OF INVENTION: Proteins that Interact with Nuclear Matrix
TITLE OF INVENTION: Proteins and Function as Transcriptional Activators
FILE REFERENCE: CL-1321
CURRENT APPLICATION NUMBER: US/09/187,999A

CURRENT FILING DATE: 1998-11-06

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Microsoft Office 97

SEQ ID NOS: 39
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APPLICANT: Stewart, Thomas S
APPLICANT: Flores, Maria V
APPLICANT: O'SUllivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                    7.6%; Score 40; DB 4; Length 1544;
53.1%; Pred. No. 0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47-80
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08446855A Patent No. 5849573 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Lycopersicon esculentum
US-09-187-999-14
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INFORMATION FOR SEQ ID NO: 1:
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703-816-4100
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                 RESULT 5
US-09-187-999-14/c
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STATE: Vi
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-08-446-855A-1
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TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996
TITLE OF INVENTION: Synthetase II
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                                                                                                                                                               7.5%; Score 39.8; DB 2; Length 8920;
49.7%; Pred. No. 0.35;
iive 1; Mismatches 98; Indels 0
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Pred. No. 0.35;
1; Mismatches 98; Indels 0
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CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-07-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09150741
Patent No. 6183996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 TACRTGTTCTTCTAA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 711 TAAATATAAATGTATAA 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-150-741-1
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Best Local Similarity 49.7%;
Matches 98; Conservative
LENGTH: 8920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                          Best Local Similarity 49.7
Matches 98; Conservative
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APPLICATION NUMBER: 60/047,618
FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                        85; Conservative
                                                                                                                                                           TYPE: DNA
ORGANISM: Thuja plicata
                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (25)..(591)
US-09-475-316A-20
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 85; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-149-476-208/c
                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                            FEATURE:
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GENERAL INFORMATION:

APPLICANT: Lewis, No. 6210942man G.

APPLICANT: Davin, Laurence B.

APPLICANT: Dinkova-Kostcva, Albena T.

APPLICANT: Gang, David R.

APPLICANT: Sarkanen, Simo

APPLICANT: Sarkanen, Simo

APPLICANT: Sarkanen, Simo

APPLICANT: Ford, Joshua D

TITLE OF INVENTION: RECOMBINANT PINORESINOL/LARICIRESINOL REDUCTASES,

TITLE OF INVENTION: RECOMBINANT DIRIGENT PROTEINS AND METHODS OF USE

FILE REFERENCE: WSUR-1-13793

CURRENT APPLICATION NUMBER: 09/9107,653

PRIOR FILING DATE: 1999-12-30

PRIOR FILING DATE: 1999-05-07

PRIOR APPLICATION NUMBER: PCT/US97/20391

PRIOR APPLICATION NUMBER: PCT/US97/20391

PRIOR APPLICATION NUMBER: 60/054.380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 ATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTATTCCCAA
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                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: P2032P1
CURRENT APPLICATION NUMBER: US/09/904,615
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/511,554
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR PILING DATE: 1998-08-25
PRIOR PILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE
LOCATION: (63)
SOTHER PROBRATION: n equals a,t,g, or C
US-09-904-615-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 AAAGCAACGCTTGAAAAAAGGAAA 169
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LOCATION: (31)
OTHER INFORMATION: n equals a,t,g, or
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US-09-475-316A-20/c
Sequence 20, Application US/09475316A
; Patent No. 6210942
                                                                                     US-09-904-615-66
; Sequence 66, Application US/09904615
Sequence 56, Application US/09904615
; Settent No. 6566325
; GENERAL INFORMATION:
711 TAAATATAAATGTATAA 727
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Best Local Similarity 54.2%
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
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913 TAAACAGCCAAAATACATTATTCTCAACTTACAAGACTCTCCAAATACTTAACAATTATC 754
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                                                                                                                                                                                                                                                                                                                                                                                                                                         7.4%; Score 39.4; DB 3; Length 873; 52.8%; Pred. No. 0.16; tive 0; Mismatches 76; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 AGCAACGCTTGAAAAAGGAAAGTTAGCCCTATCGGGTATA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                753 agradcacrcgragagrgrgargrradccrcacgaggaa 713
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FILE REPERBNCE: PZ002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT PILING DATE: 1998-09-08
CURRENT PILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER PILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER PILING DATE: 1997-03-07
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R APPLICATION NUMBER: 60/047,600
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,615
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,633
FILING DATE: 1997-05-23
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PILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,336
FILING DATE: 1997-03-07
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PRIOR FILING DATE: 1997-07-31
PRIOR APPLICATION VUMBER: 60/030,522
PRIOR FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 208, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
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R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,596
RR APPLICATION NUMBER: 60/047,612
RR APPLICATION NUMBER: 60/047,612
RR PILING DATE: 1997-05-23
RR PILING DATE: 1997-05-23
RR PILING DATE: 1997-05-23
RR PILING DATE: 1997-05-23
RR PILING DATE: 1997-05-23
RR RPILING DATE: 1997-05-23 ER APPLICATION NUMBER: 60/043,580
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,568
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,314
ER PILING DATE: 1997-04-11
ER PELLING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,311
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,671
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,671
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,671
ER FILING DATE: 1997-04-11
ER FILING DATE: 1997-04-11
ER FILING DATE: 1997-04-11 ER FILING DATE: 1997-04-11

ER PLING DATE: 1997-04-11

ER PLING DATE: 1997-04-11

ER APPLICATION NUMBER: 60/043,312

ER FILING DATE: 1997-04-11

ER APPLICATION NUMBER: 60/043,313

ER APPLICATION NUMBER: 60/043,313

ER APPLICATION NUMBER: 60/043,313

ER APPLICATION NUMBER: 60/043,573

ER FILING DATE: 1997-04-11

ER APPLICATION NUMBER: 60/043,315

ER APPLICATION NUMBER: 60/043,315

ER APPLICATION NUMBER: 60/043,974

ER PILING DATE: 1997-04-11

ER APPLICATION NUMBER: 60/048,974

ER PILING DATE: 1997-06-05 R APPLICATION NUMBER: 60/047,581
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,584
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,500
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23 R APPLICATION NUMBER: 60/056,893
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,630
R APPLICATION NUMBER: 60/056,878
R APPLICATION NUMBER: 60/056,878
R APPLICATION NUMBER: 60/056,878
R APPLICATION NUMBER: 60/056,662 LING DATE: 1997-05-23
PLICATION NUMBER: 60/047,592
LING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,613 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,582 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/056,882 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,637 APPLICATION NUMBER: 60/047,503 APPLICATION NUMBER: 60/047,598 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/056,886 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,877 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 FILING DATE: 1997-08-22 BARLIER |
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R APPLICATION NUMBER: 60/056,879
R PILLING DATE: 1997-08-22
R PILLING DATE: 1997-08-22
R PELLING DATE: 1997-08-22
R R PELLING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,894
R FILLING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,911
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,636
R FILING DATE: 1997-08-22 R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/057,761
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/047,595
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,599 R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,594

R FILING DATE: 1997-05-23

R PILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,599 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,845 FILING DATE: 1997-08-22 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,588
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,585
FILING DATE: 1997-05-23 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,614
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,903 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,888 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,910 FILING DATE: 1997-08-22
APPLICATION UNMBER: 60/056,864
LING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,631 APPLICATION NUMBER: 60/047,586 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,590 APPLICATION NUMBER: 60/043,576 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/047,501 APPLICATION NUMBER: 60/043,670 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,632 APPLICATION NUMBER: 60/056,862 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,887 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,892 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,664 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,909 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,876 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,881 FILING DATE: 1997-08-22 FILING DATE: 1997-05-23 FILING DATE: 1997-08-2 BARLIER
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R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,587

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,492

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,598

R PILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,598

R APPLICATION NUMBER: 60/047,598

R APPLICATION NUMBER: 60/047,598

R PILING DATE: 1997-05-23

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R APPLICATION NUMBER: 60/043,312
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,313
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,672
R RILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,315
R R PILING DATE: 1997-04-11
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R PILING DATE: 1997-08-22
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R PELING DATE: 1997-08-28
R PELING DATE: 1997-08-28
R PILING DATE: 1997-08-28
R APPLICATION NUMBER: 60/056,899
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,674
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,669
                                                                                                                                FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,592
FILING DATE: 1997-05-23
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APPLICATION VUMBER: 60/047,632
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,601
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APPLICATION NUMBER: 60/043,580
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APPLICATION UNMBER: 60/043,314
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,569
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APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/047,500
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APPLICATION NUMBER: 60/047,612
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APPLICATION NUMBER: 60/043,568
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,584
                                                                     1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1293 ACTCTGATAAATTTATTAAAATAAGAACAAGCATCAGTTGTACATAGAAATAATCATTTG 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 ITTATATGCTGATTTATGGGTGATTTTGCTTCCTTTGTTATACTTTTATTTTTATTCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 AAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1173 ATATCGGTTAAGGCACTATAATCCTGTCTCATGTTTTCAATAATATG 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; DB 4; Length 1378; 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 ACTACRIGITCTTCTAAGICCCACTCCTCTGTTTTCTTTGAGCAGG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.3%; Score 38.8; DB 4; 347.8%; Pred. No. 0.29; 1ive 1; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPELICATION: 186 Human Secreted proteins TILE OF INVENTION: 186 Human Secreted proteins TILE NEFERENCE: P2002P1
CURRENT FILING DATE: 1998-09-08
CURRENT FILING DATE: 1998-09-08
EARLIER PILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
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                           EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/048,964

EARLIER PILING DATE: 1997-06-06

EARLIER PILING DATE: 1997-06-06

EARLIER PILING DATE: 1997-09-05

EARLIER PILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/056,884

EARLIER PILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-09-05

EARLIER FILING DATE: 1997-06-13

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APPLICATION NUMBER: 60/056,908
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Patent No. 6420526
GENERAL INFORMATION:
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Matches 109; Conservative
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APPLICATION NUMBER: 60/047,614
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,576
FILING DATE: 1997-04-11
                             LING DATE: 1997-08-22
PLICATION NUMBER: 60/056,882
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LING DATE: 1997-08-22
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LING DATE: 1997-08-22
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G DATE: 1997-05-23
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LICATION NUMBER: 60/047,588
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G DATE: 1997-05-23
APPLICATION NUMBER: 60/056,872
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PLICATION NUMBER: 60/056,894
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PLICATION NUMBER: 60/056,631
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4G DATE: 1997-05-23
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ILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/056,875
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ICATION NUMBER: 60/056,864
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APPLICANT: Morkerium, Robert G
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APPLICANT: Morkerium, Robert G
APPLICANT: Morkerium, Robert G
APPLICANT: Liston, Peter
APPLICANT: Tsang, Benjamin K
APPLICANT: Frang, Benjamin K
APPLICANT: Prang, Benjamin K
APPLICANT: Prang, Benjamin K
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT APPLICATION NUMBER: 60/017,354
EARLIER APPLICATION NUMBER: 60/010,590
EARLIER PILING DATE: 1996-04-26
EARLIER PILING DATE: 1996-11-14
EARLIER PILING DATE: 1996-11-14
EARLIER FILING DATE: 1996-11-14
EARLIER FILING DATE: 1997-02-13
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Pred. No. 0.36;
1; Mismatches 118; Indels 0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 5232
                                                       FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,908
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/048,964
FILING DATE: 1997-06-06
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FILING DATE: 1997-09-05
APPLICATION NUMBER: 60/056,884
FILING DATE: 1997-08-22
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FILING DATE: 1997-06-13
APPLICATION NUMBER: 60/061,060
FILING DATE: 1997-10-02
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FILING DATE: 1997-09-05
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                 1997-08-22
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                 FILING DATE: 1997-08
APPLICATION NUMBER:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (4623)...(4623)
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Best Local Similarity 47.8'
Matches 109; Conservative
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GENERAL INFORMATION:
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APPLICANT: MacKenzie, Alexander B
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APPLICANT: Liston, Peter
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APPLICANT: Baird, Stephen
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                                                                                                                                                                                                                                                                                                                                                        Gapa
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US-08-545-196B-10/C
US-08-545-196B-10/C
; Sequence 10, Application US/08545196B
; Patent No. 6080577
; GENERAL INFORMATION:
; APPLICANT: MELKI, JUDITH
; APPLICANT: MUNNICH, ARNOLD
; TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                     Score 38.8; DB 3; Length 5232;
Pred. No. 0.52;
0; Mismatches 37; Indels 0
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Pred. No. 0.52;
0; Mismatches 37; Indels 0
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    ; LOCATION: 1...5232
; OTHER INFORMATION: N at 4622 and 4633 can be A, US-08-800-929A-3
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CTHER INFORMATION: n can be any nucleotide
NAME/KEY: variation
LOCATION: (4622) ... (4622)
COTHER INFORMATION: n can be any nucleotide
US-09-617-053A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09617053A Patent No. 6300492
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Best Local Similarity 62.2%;
Matches 61; Conservative
                                                                                                                                                                              Query Match 7.3%;
Best Local Similarity 62.2%;
Matches 61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-617-053A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 GCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAATTTTTCT 93
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                                                                                                                                                                                                                                                                                                  Score 38.8; DB 3; Length 5232;
Pred. No. 0.52;
0; Mismatches 37; Indels 0;
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MEDIUM TYPE: Disketre
COMPUTER: Disketre
COMPUTER: Disketre
COMPUTER: DISKETRE
OPERATIOS SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 14-NOV-1996
APTONNEY, AGENT INPORMATION:
NAME: Blaker-Brady, Kristina
REGISTRATION NUMBER:
COMPUTED TO NUMBER:
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COMPUTED TO NUMBER:
COMP
                                                                            NAME/KEY: variation
CCATION: (4622)
DCATION: (4622)
OTHER INFORMATION: n can be any nucleotide
US-09-212-911-3
OTHER INFORMATION: n can be any nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Teang, Benjamin K
APPLICANT: Pratt, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
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176 Federal Street
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TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                  7.3%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 5232 base pairs
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Best Local Similarity 62.47
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STRANDEDNESS: single
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ADDRESSEE: Clark & E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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NAME/KEY: Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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GENERAL INFORMATION:
APPLICANT: SHAO, Wei et al
APPLICANT: SHAO, Wei et al
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOH198
CURRENT APPLICATION NUMBER: US/09/820,005
CURRENT APPLICATION NUMBER: US/09/820,005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 3; Length 1582;
Pred. No. 0.51;
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                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,196B FILING DATE: 19-0CT-1995 CLASSIFICATION: 435
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Best Local Similarity 50.5%; Pred. No. 1.5;
Matches 92; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 18853
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; OTHER INFORMATION: n = A,T,C or G
US-09-820-005-3
                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION UNDHERE: 32,350
REFERENCE/DOCKET: 32,350
REFERENCE/DOCKET: 2121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8000
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09820005
Patent No. 6489149
IBM PC compatible
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Best Local Similarity 50.5%;
Matches 92; Conservative (
                                                                                                                                                                                                                                                                                                                                                                       1582 base pairs
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-545-1968-12
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AC 1377
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ORGANISM: Human
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US-09-820-005-3/c
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APPLICANT: MELKI, JUDITH
APPLICANT: MELKI, JUDITH
APPLICANT: MUNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 1582;
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,196B
FILING DATE: 19-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FARACT, C. J.
REGISTRENCE/DOCKET NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
SECHERATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                         ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP: PO BOX 747
FALLS CHURCH
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Pred. No. 0.51;
0; Mismatches
                                                                                                                                   COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 16
US-08-545-196B-12/c
; Sequence 12, Application US/08545196B
; Patent No. 6080577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.2%;
Best Local Similarity 50.5%;
Matches 92; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1582 base pairs
NUMBER OF SEQUENCES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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STATE: VI
COUNTRY:
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,315
FILING DATE: 1997-04-11
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                                                          1997-03-07
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                                                                                     PPLICATION NUMBER:
15117 GGTTTGTTTTTTTTTTTTTTTTCAGTAIGAAATCCATCTGTTCCAGCACC 15058
                                                                                                                     14997 AAAAGAAAACTTTGCATAATACAAGGTTCACATAAAACCCAATTCTTGGCTGGTGGGGGG 14938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 GADAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 TICTITATACTITIATITATICCCAAATITITICTTAAGCAAATATTTCTTTGCTAATCAA 119
                                                                                AATITITICITIAAGCAAATATITICITIGCIAATCAATAAATTATCAAAAGAAAAAAAACT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Strauss et al.

TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in TITLE OF INVENTION: poplar and other plant species.

TITLE OF INVENTION: poplar and other plant species.

FILE REFERENCE: 53375
CURRENT PELICANION NUMBER: US/09/410,464
EARLIER FILING DATE: 1999-10-01
EARLIER FILING DATE: 1999-04-06
EARLIER FILING DATE: 1999-04-06
EARLIER FILING DATE: 1998-04-06
SARLIER FILING DATE: 1998-04-06
SOFTWARE: PARENCE: 2.0
SEQ ID NO 5: 24
LENGTH: 5656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 TAAATTATCAAAAGAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTT 172
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TITLE OF INVENTION: 186 Human Secreted proteins
FILE REPERENCE: P2002P1
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER PILING DATE: 1998-03-06
EARLIER PILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-03-07
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; ORGANISM: Populus balsamifera subsp. trichocarpa
US-09-410-464-5
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US-09-149-476-66
'Sequence 66, Application US/09149476
'Patent No. 6420526
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09410464
Patent No. 6395892
                                                                                                                                                                                                                                                                                                                                      14937 AT 14936
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R FILING DATE: 1997-03-07
R APPLICATION NUMBER: 60/047,600
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,615
R PILING DATE: 1997-05-23
R PELING DATE: 1997-05-23
R FILING DATE: 1997-05-23
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R PAPLICATION NUMBER: 60/047,617
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,618
R APPLICATION NUMBER: 60/047,503
R APPLICATION NUMBER: 60/047,503
R PILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,601
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,580
FILING DATE: 1997-04-11
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,500
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APPLICATION NUMBER: 60/047,492
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APPLICATION NUMBER: 60/047,598
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,582
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APPLICATION NUMBER: 60/043,314
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APPLICATION NUMBER: 60/043,669
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                                                                                                                                                                                                               FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,633
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APPLICATION NUMBER: 60/047,583
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APPLICATION NUMBER: 60/047,584
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APPLICATION NUMBER: 60/047,587
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APPLICATION NUMBER: 60/047,632
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EARLIER APPLICATION NUMBER: 60/056,911
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
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EARLIER PLILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/047,590
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER PILING DATE: 1997-05-23
EARLIER PILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER RELING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,693
EARLIER RELING DATE: 1997-05-23
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RETLING DATE: 1997-08-22
RE APPLICATION NUMBER: 60/056, 637
RE FILING DATE: 1997-08-22
RE APPLICATION NUMBER: 60/056, 903
RE FILING DATE: 1997-08-22
RE APPLICATION NUMBER: 60/056, 888
RETLING DATE: 1997-08-22
RE APPLICATION NUMBER: 60/056, 889
RETLING DATE: 1997-08-22
RE APPLICATION NUMBER: 60/056, 880
RETLING DATE: 1997-08-22
RE APPLICATION NUMBER: 60/056, 880
RETLING DATE: 1997-08-22
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,889
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,893
R RILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,630
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,625
R R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,662
R R FILING DATE: 1997-08-22
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                                                              FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/056,886
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/043,578
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,576
APPLICATION NUMBER: 60/048,974
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.. 0 7.1%; Score 37.6; DB 4; Length 732; 56.5%; Pred. No. 0.46; ive 0; Mismatches 54; Indels ER FILING DATE: 1997-04-11

ER APPLICATION NUMBER: 60/056,632

ER FILING DATE: 1997-08-22

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,876

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,891

ER APPLICATION NUMBER: 60/056,909

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,909

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,875

ER FILING DATE: 1997-08-22

ER APPLICATION NUMBER: 60/056,875

ER FILING DATE: 1997-08-22

ER FILING DATE: 1997-08-22

ER FILING DATE: 1997-08-22

ER FILING DATE: 1997-08-22

ER FILING DATE: 1997-08-22

ER FILING DATE: 1997-08-22

ER FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,501 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/043,670 EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02 FILING DATE: 1997-08-22
APPLICATION UNMBER: 60/048,964
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/057,650 APPLICATION NUMBER: 60/056,884 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/057,669 FILING DATE: 1997-09-05 FILING DATE: 1997-04-11 Best Local Similarity 56.5 Matches 70; Conservative 166 GAAA 169 Query Match BARLIER
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RESULT 20

Sequence 1, Application US/09013810
Patent No. 6197551
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: No. 6197551el TANGO 80 Molecules and Uses Thereof NUMBER OF SEQUENCES: 9
CORRESPONDENCES: ADMING & COCKFIELD, LLP
STREET: 28 State Street CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 US-09-013-810-1/c

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US-09-601-198-165
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US-08-916-421B-1
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APPLICANT: Williamson, Richard E.
APPLICANT: Williamson, Richard E.
APPLICANT: Berzner, Andreas S.
APPLICANT: Berzner, Andreas S.
APPLICANT: Berzner, Andreas S.
APPLICANT: Berzner, Liangeai TITLE OF INVENTION: Manipulation of cellulose and/or Beta-1,4-glucan FILE OF INVENTION: Manipulation of cellulose and/or Beta-1,4-glucan FILE OF INVENTION WIMBER: US/09/221,013A
CURRENT APPLICATION NUMBER: PCT/AU97/00402
PRIOR APPLICATION NUMBER: PCT/AU97/00402
PRIOR APPLICATION NUMBER: AU PO0699
PRIOR FILING DATE: 1996-06-27
NUMBER: OF SEQ ID NOS: 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 7.1%; Score 37.6; DB 3; Length 746; Best Local Similarity 54.3%; Pred. No. 0.47; Matches 76; Conservative 0; Mismatches 64; Indels
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~heg 64; Indels
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,810
FILING DATE:
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Patent No. 6495740
GENERAL INFORMATION:
APPLICANT: Arioli, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147 AAGCAACGCTTGAAAAAGG 166
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                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-
TELECPHONE: (617)227-7400
TELECPHONE: (617)242-4114
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 746 base pairs
TYRE: nucleic acid
STRANBENES/SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Arabidopsis thaliana
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; LOCATION: (239)..(3490)
US-09-221-013A-7
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; LOCATION: 135..428
US-09-013-810-1
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Best Local Similarity
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SEQ ID NO 7
LENGTH: 3828
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US-09-221-013A-7
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GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococc
Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REPERENCE: 18275
CURRENT APPLICATION NUMBER: US/08/916,421B
FILOR PERIONE: 1997-08-22
FILOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
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Sequence 165, Application US/09601198

Patent No. 6531583

GENERAL INFORMATION:

APPLICANT: Casell, Gail H.

APPLICANT: Casell, Gail H.

APPLICANT: Glass, John I.

APPLICANT: Glass, John I.

APPLICANT: Glass, John I.

APPLICANT: Glass, John I.

APPLICANT: Glass, John I.

APPLICANT: Glass, John I.

APPLICANT: Glass, John I.

APPLICANT: Glass, John I.

APPLICANT: Glass, John I.

APPLICANT: Heiner, Cheryl R.

APPLICANT: Heiner, Cheryl R.

APPLICANT: Heiner, Cheryl R.

APPLICANT: Heiner, Claryl R.

APPLICANT: Honer, Claryl R.

APPLICANT: Honer, Cheryl R.

APPLICANT: Honer, Cheryl R.

FILE REFERENCE: UAB-13452/22

CURRENT PILING DATE: 1998-01-30

FRIOR PRIOR FILING DATE: 1998-01-30

NUMBER OF SEQ ID NOS: 181

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 165

LENGTH 4344
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                                                                                                         3671 ATTGTTTGTTTTTTTTTTTTTGTACTTTTTAGTTATTCCGTAGTTATTGTATAATACT 3730
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                                                       42 ATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTTCCCAAATTTTTCTTAAGCAAA 101
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Pred. No. 1;
0; Mismatches 64; Indels 0;
54; Indels
  0; Mismatches
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ORGANISM: Ureaplasma urealyticum
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Best Local Similarity 54.3
Matches 76; Conservative
70; Conservative
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SOFTWARE. DatentIn version 3 1	1664976	NA NA	OKGANISM: Methanococcus jannaschi FEATURE:	NAME/KEY: misc_feature LOCATION: (28222)(28222)	OTHER INFORMATION: n equals a, NAME/KEY: misc feature	LOCATION: (28257)(28258)	misc feature	LOCATION: (84//3)(84/73) OTHER INFORMATION: n equals a,	NAME/KEY: misc_feature LOCATION: (84808)(84808)	OTHER INFORMATION: n equals a,	LOCATION: (84812)(84812)	OTHER INFORMATION: n equals a, NAME/KEY. misc feature	ION: (98120)(98120)	OTHER INFORMATION: n equals a, NAME/KEY: misc feature	(98159)(98159)	KEY: misc feature	(98239) . (98239)	NAME/KEY: misc feature	(98266) (98266)	OTHER INFORMATION: n equals a,	LOCATION: (98343) . (98343)	OTHER INFORMATION: n equals a,	NAME/KEI: MISC rearure LOCATION: (103998). (103998)	RMATION: n equal	NAME/KEY: misc feature	RMATI	misc fea		NAME/KEY: misc feature	v	NAME/KEY: misc feature	OTHER INFORMATION: n equals a,		OTHER INFORMATION: n equals a,	NAME/KEY: misc feature	RMATION: n equal	NAME/KEY: misc feature	OTHER INFORMATION: n equals a,	NAME/KEY: misc feature	RMATION: n equal	NAME/KEY: misc_feature LOCATION: (309398)(309398)	RMATION: n equal	NAME/KEY: misc_feature LOCATION: (309418)(309418)	OTHER INFORMATION: n equals a,	12837)	OTHER INFORMATION: n equals a, NAME/KEY: misc_feature

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OTHER INFORMATION: n equals a, the NAME/KEY: misc_feature and the Locations and the Locations in the Locations and the Locati NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (1349491)..(1349491)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (1470091)..(1470091)

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STREET: One Liberty Place 46th Ploor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 7.0%; Score 37.2; DB 1; Length 5852; 1 Similarity 56.6%; Pred. No. 1.5; 69; Conservative 0; Mismatches 53; Indels 0
                                                                                             Sequence 2, Application US/07867106
Patent No. 5389526
GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Glang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 538952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILNG DATE: 19920625

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 3U PJ 7187

APPLICATION NUMBER: 3U PJ 7187

APPLICATION NUMBER: PCT/AU90/00530

FILING DATE: 02-NOV-1989

ATORNEY/AGENT INFORMATION:

NAME: FEERRATION NUMBER: 35,134

REGISTRATION NUMBER: 35,134
1424 TTTTTTTTYKTTGAAACCAATAATTTATCAAAA 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE DOCKET NUMBER: RICE-0002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 5852 base pairs
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2378..5038
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Best Local Similarity
Matches 69; Conserva
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LOCATION:
FEATURE:
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                      CITY: Phi
STATE: PA
COUNTRY:
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; LOCATION:
US-07-867-106-2
                                                                                           US-07-867-106-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 TGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 TGATTIATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTTTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 1664976;
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.1%; Score 37.6; DB 4; Length 16
Best Local Similarity 50.6%; Pred. No. 15;
Matches 91; Conservative 0; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: 44 Human Secreted Proteins
FILE REFERENCE: PZ024P1
                                                                               | NAME/KEY: misc feature | CATION: (1602912) | OTHER INFORMATION: (1602912) | OTHER INFORMATION: (1603734) | OTHER INFORMATION: n equals a, t, c, or g | NAME/KEY: misc feature | CATION: (1603734) | OTHER INFORMATION: n equals a, t, c, or g | NAME/KEY: misc feature | CATION: (1637998) | CATION: (1649598) | CATION: (1664959) | OTHER INFORMATION: n equals a, t, c, or g | US-08-916-4218-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE KEKERMENE: FUGGATE,
CURRENT PELING DATE: 1999-08-05
CURRENT FILING DATE: 1999-08-05
EARLIER APPLICATION NUMBER: 60/074,118
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
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EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 172
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/09369247
Patent No. 6569992
GENERAL INFORMATION:
                NAME/KEY: misc feature
LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a,
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.0°
Best Local Similarity 60.6°
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-369-247-23
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ATTORNEY/AGENT INFORMATION:
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Matches 70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08545196B
Patent No. 6080577
GENERAL INFORMATION:
APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIYAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCE: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 717
CITY: FALLS CHURCH
                                                      GENERAL INFORMATION:
APPLICANT: MELKI, JUDITH
APPLICANT: MUNNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.0%; Score 37; DB 3; Length 1582; 56.0%; Pred. No. 0.95; tive 0; Mismatches 55; Indels
                                                                                                                                                                                                             ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP
STREET: PO BOX 747
CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,196B FILING DATE: 19-OCT-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 19-OCT-1995
CLASSIFICATION: 435
ATTORNEY, FAGENT INFORMATION:
NAME: FARACI, C. J.
REGISTRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 2121-110P
TELEPHONE: (703) 205-8050
TELEPHONE: (703) 205-8050
TELEPAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  Sequence 10, Application US/08545196B Patent No. 6080577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1582 base pairs
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Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                  ADDRESSEE:
US-08-545-196B-10
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US-08-545-196B-12
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COUNTRY: 2040-074

ZIL: 2040-074

COMPITER READMLE FORM:

MEDIUMY TIPE: 1200PG diek

SOCRETARE PREADMLE FORM:

MEDIUMY TIPE: 1200PG diek

SOCRETARE PREADMLE FORM:

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36, Application US/09005051 Patent No. 6291222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2007 nucleotides
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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                     TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-747-221B-38
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Best Local Similarity
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                               5 AAAAA 1
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MOLECULE TYPE:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-005-051-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-005-051-36
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Patent No. 6063610
GENERAL INFORMATION:
APPLICANT: SILVEr, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.0%; Score 37; DB 3; Length 2007; Best Local Similarity 56.0%; Pred. No. 1.1;. Matches 70; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordberfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,221B
FILING DATE: No. 6063610ember 12, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Carol Talkington Verser, Ph.D. ADDRESSEE: Heska Corporation STREET: 1825 Sharp Point Drive CITY: Fort Collins STATE: Colorado COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
Verser, Carol Talkington
          REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: FC-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/484-9505
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 2007 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: FC
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2007 nucleotides
TYPE: nucleic acid
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                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003 AAAAA 2007
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                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IS-08-747-221B-38/C
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US-08-747-221B-36
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                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Silver, Gary W.
APPLICANT: Silver, Gary W.
APPLICANT: Wienewski, No. 6791222el Carboxylesterase Nucleic Acid TITLE OF INVENTION: Molecules, Proteins and Uses Thereof NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heska Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STREET: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.0%; Score 37; DB 3; Length 2007; 56.0%; Pred. No. 1.1;
DB 3; Length 2007;
Query Match 7.0%; Score 37; DB 3; Length 200° Best Local Similarity 56.0%; Pred. No. 1.1; Matches 70; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
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518 ririringitaaaarriaringcaragraaarritaagritaaacccaacaaccaactaactrar 577
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                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Artiushin, Sergey
APPLICANT: Stipkowits, Laslo
APPLICANT: Minion, F. Chris
TITLE OF INVENTION: PCR-Based Assay For Mycoplasma
TITLE OF INVENTION: Hyopneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC_COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB :
Pred. No. 1.1;
0; Mismatches
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dickstein, Shapiro and Morin
STREET: 2101 L. St. NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Thomas Jefferson University
APPLICANT: Raphael Rubin
APPLICANT: Manorama Tewari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/062,632
FILING DATE: 18-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 AGCAACGCTTGAAAAAAGGAA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   578 AAAACCGAAAGGAATTAGTAA 598
                                                                                                                               Sequence 4, Application US/08062632
Patent No. 5712090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09234245
Patent No. 6509457
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: I
TELECOMMUNICATION INFORMATION
TELEPHONE: (202)785-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Brady Jr., James W.
REGISTRATION NUMBER: 32,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2334 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (202)887-0689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 53.9
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                        Washington
 144 TGAAA 148
                                                                                                                                                                                                                                                                                                                                                  CITY: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 18 CLASSIFICATION:
                                      5 AAAAA 1
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US-09-234-245-1
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                                                                                                                                                 24 IGATTIATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTATTCCC 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 TGATTTATATGCTGATTTATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCC
 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Silver, Gary W.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid
TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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Pred. No. 1.1;
0; Mismatches 55; Indels
55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carol Talkington Verser, Ph.D.
Heska Corporation
 Mismatches
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APPLICATION NUMBER: 08/747,221
FILING DATE: No. 6291222ember 12, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Verser, Carol Talkington REGISTRATION NUMBER: 37,459
                                                                                                                                                                                                                                                                                                                   Sequence 38, Application US/09005051
Patent No. 6291222
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56.0%;
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Best Local Similarity که ۱۳۰۰
استامه ۲۵٫ Conservative
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INFORMATION FOR SEQ ID NO:
 70; Conservative
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ADDRESSEE: Carol Tall
ADDRESSEE: Heska Cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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US-09-005-051-38/c
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Gaps

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92; Indels

Pred. No. 3.1; 0; Mismatches

50.04;

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40 TIATGGGTGATTTTGCTTCCTTCTTTATACTTTTATTTCCCAAATTTTTCTTAAGCA
                          92; Conservative
  Best Local Similarity
Matches 92; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 AAATTATCAAAAGAAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                 DB 4; Length 3715;
TITLE OF INVENTION: Compositions And Methods For Modulating TITLE OF INVENTION: Apoptosis FILE REFERENCE: TUU-002 CURRENT APPLICATION NUMBER: US/09/234,245 CURRENT APPLICATION NUMBER: US 60/071,878 EARLIER APPLICATION NUMBER: US 60/071,878 EARLIER FILING DATE: 1998-01-20 SOFTWARE: FastSEQ for Windows Version 3.0 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                           61 TCTTTATACTTTTATTTCCCAAATTTTTCTTAAGCAAATATTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891 FILING DATE: 2-DEC-1996 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                       45;
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GLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
""TRPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                               Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Wulligan, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schallenberg, Gerald D.
TITLE OF INVENTION: GENE PROI
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 208, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Yu, Ying-Hui
APPLICANT: Yu, Chang-En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                             7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         209
                                                                                                                                                                                                                                                                                                                                     Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                      , ORGANISM: Mus musculus US-09-234-245-1
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Washington
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                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-781-891-208
                                                                                                                                                                                                LENGTH: 3715
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Best Local S
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7.0%; Score 36.8; DB 3; Length 16442;

Query Match

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14571 CAAATTTCATTTTAGATTTTGAAAAGATTGTATAGGTTTAAAACCTCTCAATTTCATTACA 14630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPACTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/618,166
FILING DATE: 17-011-2000
CLASSIFCATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fu, Ying-Hui
Yu, Chang-En
Oshima, Junko
Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MCMGGLETG, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.0%; Score 36.8; DE 50.0%; Pred. No. 3.1; tive 0; Mismatches
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TOPOLOGY: linear
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SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-09-618-166-208
                                                                                                                                                                                                                                                                                                                                      Sequence 208, Application US/09618166
Patent No. 6581112
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed In
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Best Local Similarity
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US-09-453-323-1
                                                                                                                                                                                                                                                                               TYPE: DNA
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                                           14571 CAAATTTCATTTTAGATTTTGAAAAGATTGTATAGGTTTAAACCTCTCAATTTCATTACA 14630
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160 AAAAAGGAAAGTTAGCCCTATCGGGTATATTTTGGAAGTTGTAAAATACTACRTGTTCTC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             975 rititititititititititititinaaaantaaaahtchittaaaaaaaa 923
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                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TILE REPERENCE: PZ031P1
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER PEPLICATION NUMBER: PCT/US99/17130
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-105
EARLIER FILING DATE: 1998-08-105
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
SEARLIER FILING DATE: 1998-08-06
SEARLIER FILING DATE: 1998-08-06
SOFTWARE: PALCATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
SOFTWARE: PALCATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
SOFTWARE: PALCATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
SOFTWARE: PALCATION NUMBER: 60/095,455
EARLIER FILING DATE: 1998-08-06
SOFTWARE: PALCATION NUMBER: 60/095,455
SEQID NOS: 376
SEQID NOS: 376
SEQID NOS: 376
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Patent No. 6476195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (951)
; OTHER INFORMATION: n equals a,t,g,
US-09-489-847-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (936)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
LOCATION: (946)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                             14691 TTGT 14694
                                                                                                                                                                                    220 TTCT 223
                                                                                                                                                                                                                                                                                                   RESULT 36
US-09-489-847-112/c
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US-08-894-731-2
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; Sequence 2, Application US/08894731; Patent No. 6084089; GENERAL INFORMATION:

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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 TTTATACTTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09453323

Patent No. 641272

GENERAL INFORMATION:
APPLICANT: Ye, Zheng-Hua
TITLE OF INVENTION: MODIFICATION OF LIGNIN CONTENT AND COMPOSITION IN
TITLE OF INVENTION: PLANTS

FILE REFERENCE: 235.00090101
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APPLICANT: OHYMA, AKIO.
APPLICANT: HYDOSH, Toru.
APPLICANT: HYSOSH, Toru.
APPLICANT: KASACA, Keisuke
TITILE OF INVENTION: COLD-INDUCIBLE PROMOTER SEQUENCE
TITILE REFERENCE: 760-234P
CURRENT PILICATE: 1997-10-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 4140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.8%; Score 36.2; DB 4;
ilarity 57.5%; Pred. No. 0.77;
Conservative 0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
6.9%; Score 36.4; Di
Best Local Similarity 53.5%; Pred. No. 2.2;
Matches 76; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       346 ATCAATATAGATAATTAAATCT 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-328-352-642; Sequence 642, Application US/09328352; Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Acinetobacter baumannii US-09-328-352-642
                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Solanum tuberosum
US-08-894-731-2
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Matches 65; Conserv
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APPLICANT: Pallas, David C
APPLICANT: Du, Xianxing
TITLE OF INVENTION: Coding Sequence for Protein Phosphatase Methylesterase,
Patent No. 6232110
TITLE OF INVENTION: Recombinant DNA Molecules and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2300 icifigitatianganchiginnaakgaaantaanchcccaacchiaaaaaaa 2359
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TITLE OF INVENTION: Coding Sequence for Protein Phosphatase Methylesterase,
TITLE OF INVENTION: Coding Sequence for Protein Phosphatase Methylesterase,
Patent No. 6528295
TITLE OF INVENTION: Recombinant DNA Molecules and Methods
FILE REFERENCE: Docket No. 6528295 105-97A
CURRENT APPLICATION NUMBER: 05/09/839, 497A
CURRENT FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 60/082, 202
PRIOR PILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/293, 322
RIOR PILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 TTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 TTTTATTTATTCCCAAATTTTTCTTAAGCAAATATTTCTTTGCTAATCAATAAATTATCA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 3; Length 2409;
Pred. No. 2.2;
0; Mismatches 40; Indels
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; Pred. No. 2.2;
0; Mismatches
                                                                                                                                                                         CURRENT APPLICATION NUMBER, US/09/293,322C
CURRENT APPLICATION NUMBER, US/09/293,322C
CURRENT FILING DATE: 1999-04-16
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 2409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature

LOCATION: (1)..(2409)

OTHER INFORMATION: N is A, T, G or C.

US-09-293-122C-8
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; OTHER INFORMATION: N 16 A, T, G or C.
US-09-839-497A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/09839497A Patent No. 6528292 GENERAL INFORMATION: APPLICANT: Pallas, David C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.8%;
Best Local Similarity 60.0%;
Matches 60; Conservative
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Best Local Similarity 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Mus musculus
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                                    GENERAL INFORMATION:
APPLICANT: Pallas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-839-497A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                           DB 4; Length 1507;
                                                                                                                                                                                                                                                                                                                                                             55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 59 Application US/08821994A
; Sequence 59. Application US/08821994A
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Greenland, Andrew J
APPLICANT: Thomas, Didier RP
APPLICANT: Thomas, Didier RP
; APPLICANT: Jepson, Ian
TITLE OF INVENTION: Promoters
; FILE REFERENCE: PDD 50108
; CURRENT APPLICATION WUMBER: PCT/GB97/00729
; EARLIER APPLICATION NUMBER: PCT/GB97/00729
; EARLIER PILING DATE: 1997-03-18
; EARLIER FILING DATE: 1997-03-18
; EARLIER FILING DATE: 1996-03-22
; NUMBER OF SEQ ID NOS: 89
; SCQ ID NO 59
; LENGTH: 1577
**TYPE: NNA
                                                                                                                                                                                                                                                                                                      ch 6.8%; Score 36; DB 4
1 Similarity 55.6%; Pred. No. 1.8;
69; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1546 AAAAAAAAAAAAAAAAAAAAAAAAAA 1573
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CURRENT APPLICATION NUMBER: US/09/453,323
CURRENT FILING DATE: 1999-12-02
PRIOR PILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
LENGTH: 1507
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US-09-293-322C-8
; Sequence 8, Application US/09293322C
                                                                                                                                                                                                        TYPE: DNA ORGANISM: Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Brassica napus
US-08-821-994-59
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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US-08-821-994-59
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3581 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
284..2671
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US-08-738-349-1
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Best Local S
Matches 78
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                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Cassell, Gail H.
APPLICANT: Cassell, Gail H.
APPLICANT: Cassell, Gail H.
APPLICANT: Cassell, Gail H.
APPLICANT: Glass, John I.
APPLICANT: Helmer, Cherryl R.
APPLICANT: Helmer, Cherryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: UNELLY ALION
TITLE OF INVENTION: UNELLY ALION
FILE REFERENCE: UAB-13452/22
CURRENT APPLICATION NUMBER: US/09/601,198
FILE REPERENCE: UAB-13452/22
CURRENT APPLICATION NUMBER: 60/073,189
FRIOR APPLICATION NUMBER: 60/073,189
FRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 102
LENGTH: 3165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2158 IGTITIGAICAIATICAAGITCITIACITGIGAITICAGGCITGCIAAICCCAIAITIAA 2099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 ACTITITATITATICCCAAATITITICTIAAGCAAATATITICTITGCTAATCAATAAATTAT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 CAAAAGAAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAAGTTAGCCCTATCGGGTAT 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Takeshita, Sunao
APPLICANT: Ckazaki, Makoto
APPLICANT: Kawai, Shinji
APPLICANT: Rawai, Shinji
APPLICANT: Tsujimura, Atsushi
APPLICANT: Amain, Egon
TITLE OF INVENTION: Bone-Related Cadherin-Like Protein and
TITLE OF INVENTION: Process for Its Production
CORRESPONDENCE: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
6.8%; Score 36; DB 4; Length 3165;
Best Local Similarity 47.7%; Pred. No. 2.5;
Matches 105; Conservative 0; Mismatches 115; Indels
                                         2038 CAİCTAAAAGİTTITTAATATİTTCTTTATTTCAATTAĞİ 1999
  130 AAAGAAAAAAACTGAAAGCAACGCTTGAAAAAAGGAAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 ATTITGGAAGTIGTAAAATACTACRIGTICTCTTCTAAGT 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                         Sequence 102, Application US/09601198
Patent No. 6531583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/08738349; Patent No. 5869638; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Ureaplasma urealyticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1300 I Street, N.W. CITY: Washington STATE: D.C.
                                                                                                           RESULT 43
US-09-601-198-102/c
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3521 Trititititititititititaaaaakgaarcirititititatricaaaggirgcricitarar 3462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 6.8%; Score 36; DB 2; Length 3581; Local Similarity 52.7%; Pred. No. 2.6; nes 78; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 GTAGTCGTGGCTGATTTATATGCTGATTTATGGGTGATTTTGCTTCCTT
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,349
FILING DATE: 25-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/364,439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fischer et al.
TILLO WINNENNATION:
FILE REFERENCE: PZO10P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1999-07-08
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER FILING DATE: 1997-07-08
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EARLIER FILING DATE: 1997-07-08
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PPP: 02481.1323-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN: osteoblastic cell line MC3T3E1
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/112,061
APPLICATION NUMBER: US 08/112,061
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barker, M. P.
REGISTRATION NUMBER: 32,013
REFERENCE/DOCKET NUMBER: 02481.1323
TELEPONE: 202-408-4400
TELEFAX: 202-408-4400
TELEFAX: 202-408-4100
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; Sequence 76, Application US/09227357
; Patent No. 6342581
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EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/052,733
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,795
FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,948
FILING DATE: 1997-08-18
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PPLICATION NUMBER: 60/055,953
ILING DATE: 1997-08-18
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APPLICATION NUMBER: 60/055,947
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APPLICATION NUMBER: 60/055,684
PLICATION NUMBER: 60/052,803
LING DATE: 1997-07-08
                                             LICATION NUMBER: 60/052,732
                                                                                                                                                      FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/051,916
                                                                                                                                                                                                                              APPLICATION NUMBER: 60/051,930
FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/051,918
FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                        PPLICATION NUMBER: 60/051,920
ILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/051,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/055,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,723
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APPLICATION NUMBER: 60/055,964
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APPLICATION NUMBER: 60/056,360
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EARLIER APPLICATION NUMBER: 60/055,984
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NAME/KEY: SITE
LOCATION: (13)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1997-08-18
                                                                                                                                                                                                             ILING DATE: 1997-07-08
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ORGANISM: Homo sapiens
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LENGTH: 519
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DUCATION: (24) OTHER INFORMATION: n equals a,t,g, or FEATURE:

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